

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 30, 2004, 12:18:33 ; Search time 54 Seconds
(without alignments)
2579,554 Million cell updates/sec

Title: US-10-018-386-2
Perfect score: 2682
Sequence: 1 MRPLCTCMTGLIAGAGV.....GSYSLKRVMMIRNPVTFH 493

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2686	100.0	493	4	AAB66340
2	2682	99.9	493	2	AAY05396 Human ang
3	2682	99.9	493	3	AAY54999 Human TIE
4	2682	99.9	493	3	AAY70745 FSEQ-3 pr
5	2682	99.9	493	3	AAB47997 Angiopoie
6	2682	99.9	493	4	AAB31179 Amino aci
7	2682	99.9	493	4	AAB12305 Human PRO
8	2682	99.9	493	4	AAB51329 Human 410
9	2682	99.9	493	5	AA014786 Human mat
10	2682	99.9	493	5	ABG80355 Human TIE
11	2682	99.9	493	5	AAE19825 Human TIE
12	2682	99.9	493	5	AB017749 Novel hum
13	2682	99.9	493	6	AB025150 Novel hum
14	2682	99.9	493	6	ADN01417 Human ang
15	2682	99.9	493	6	AB081003 Human PRO
16	2682	99.9	493	6	AAE32417 Human ang
17	2682	99.9	493	6	ABU66703 Human PRO
18	2682	99.9	493	6	ABU67268 Novel hum
19	2682	99.9	493	6	ABU59784 Novel sec
20	2682	99.9	493	6	AB024974 Human sec
21	2682	99.9	493	6	ABU72036 Novel hum
22	2682	99.9	493	6	ABU67137 Novel hum
23	2682	99.9	493	6	ABU66979 Human sec
24	2682	99.9	493	6	AAE30335 Human ARP
25	2682	99.9	493	6	ABU79779 Human sec

25	2682	99.9	493	6	ADA45787	Ada45787 Novel hum
26	2682	99.9	493	6	ADA76218	Ada76218 Human PRO
27	2682	99.9	493	6	ADA18868	Ada18868 Human PRO
28	2682	99.9	493	6	ADA61491	Ada61491 Homo sapi
29	2682	99.9	493	6	ADA19276	Ada19276 Novel hum
30	2682	99.9	493	6	ADA67817	Ada67817 Human PRO
31	2682	99.9	493	6	ADA66296	Ada66296 Novel hum
32	2682	99.9	493	6	ADA15860	Ada15860 Human PRO
33	2682	99.9	493	6	ADA47646	Ada47646 Human PRO
34	2682	99.9	493	6	ADA67441	Ada67441 Human PRO
35	2682	99.9	493	6	ADA83048	Ada83048 Human PRO
36	2682	99.9	493	6	ADA85744	Ada85744 Novel hum
37	2682	99.9	493	6	ADA96956	Ada96956 Human PRO
38	2682	99.9	493	6	ADA79260	Ada79260 Human PRO
39	2682	99.9	493	6	ADA87399	Ada87399 Novel hum
40	2682	99.9	493	6	ADA67601	Ada67601 Human PRO
41	2682	99.9	493	6	ADA81693	Ada81693 Novel hum
42	2682	99.9	493	6	ADA14756	Ada14756 Human sec
43	2682	99.9	493	6	ADA47176	Ada47176 Human sec
44	2682	99.9	493	6	ADA18717	Ada18717 Novel hum
45	2682	99.9	493	6	ADA18717	Ada18717 Novel hum

ALIGNMENTS

RESULT 1
ID AAB66340 standard; protein; 493 AA.
XX AC AAB66340;
XX DT 05-APR-2001 (first entry)
XX DE Human angiopoietin-7 (ANG-7).
XX KM Human angiopoietin-7; ANG-7; angiogenesis; cancer; wound healing;
XX KN diabetic retinopathy; macular degeneration; cardiovascular disease;
XX KW reproductive system.
XX OS Homo sapiens.
XX PN WO000102434-A1.
XX PD 11-JAN-2001.
XX PF 30-JUN-2000; 2000MO-US018170.
XX PR 02-JUL-1999; 99EP-00113502.
XX PA (FARB) BAYER AG.
XX FI Friedrich G, Hagen G, Wick M, Zubov D, Dubois-Stringfellow N;
XX PT WPI; 2001-123103/13.
XX PR N-PSDB; AAF29738.
XX PS Inhibiting angiogenesis for treating cancer, wound healing, diabetic
XX CC retinopathies, macular degeneration, cardiovascular diseases, by
XX CC administering angiopoietin-7 polypeptide or its fragments.
XX CC Claim 2; Fig 2; 86pp; English.
XX CC The present invention describes a method of preventing angiogenesis by
XX CC administering angiopoietin-7 (ANG-7) nucleic acid, protein, fragment or
XX CC derivative. This can be used in the treatment of angiogenesis-related
XX CC diseases, including cancer, wound healing, macular degeneration,
XX CC cardiovascular diseases, diabetic retinopathies, infections and
XX CC conditions of the reproductive system such as regulation of placental
XX CC vasculatization, and also may be used as an abortifacient. Note: In the
XX CC specification, ANG-7 is also referred to as being angiotensin-7
XX CC Sequence 493 AA:

Query Match 100.0%; Score 2686; DB 4; Length 493;
Best Local Similarity 100.0%; Pred. No. 6.6e-217;
Matches 493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAAMGAVAGQEDGEGTEGSGRREFTYLRKRAESQDKCTYFTIV 60
DB 1 MRPLCTCWMGLGLAAMGAVAGQEDGEGTEGSGRREFTYLRKRAESQDKCTYFTIV 60
QY 61 POORVTGATCVNSKEPEVLENRVHKQELINNELNKKQKQIETLQQLVADGIVSEV 120
DB 61 POORVTGATCVNSKEPEVLENRVHKQELINNELNKKQKQIETLQQLVADGIVSEV 120
QY 121 KILRKESRMNSRVTLQVWQLHETIRKRDNALBESQLENRIINQTAQMLQASKYKOLE 180
DB 121 KILRKESRMNSRVTLQVWQLHETIRKRDNALBESQLENRIINQTAQMLQASKYKOLE 180
QY 181 HKYQHLATLANHQSSEIIAQLEBHCQVPSARVPQPPAAPPVRYQPTYNRIINQISTN 240
DB 181 HKYQHLATLANHQSSEIIAQLEBHCQVPSARVPQPPAAPPVRYQPTYNRIINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMTLTSLSSTDKSPGPRDCLQALBDGHTSSIYLVKPEPTN 300
DB 241 EIQSDQNLKVLPPPLPTMTLTSLSSTDKSPGPRDCLQALBDGHTSSIYLVKPEPTN 300
QY 301 RLMQVWCDQRHDPGGMVTYIQRLDGSVNFPRWMEYKQGFNIDGEMWLGLENIYWLTNQ 360
DB 301 RLMQVWCDQRHDPGGMVTYIQRLDGSVNFPRWMEYKQGFNIDGEMWLGLENIYWLTNQ 360
QY 361 GNYKLLVTEWDSGKRVFAEYASFRLPESESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLLVTEWDSGKRVFAEYASFRLPESESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAHYQKGGWYNAKAHNSLNGWYRGHRSRYQDGVYAAEFRGSGYSLSKK 480
DB 421 RDHDVYTGNCAHYQKGGWYNAKAHNSLNGWYRGHRSRYQDGVYAAEFRGSGYSLSKK 480
QY 481 VVMIRPNPNTFH 493
DB 481 VVMIRPNPNTFH 493

RESULT 2
AAV05396
ID AAV05396 standard; protein; 493 AA.

XX AAY05396;
AC AAY05396;
DT 01-JUL-1999 (first entry)
DE Human TIE ligand N1.1 protein sequence.
XX Human TIE ligand; N1.1; N1.4; N1.5; N1.8; Ig homology domain; angiogenesis;
KM EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KM early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KM endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KM vasculogenesis; detection; diagnosis; therapy.
XX
OS Homo sapiens.
XX
PN W09915653-A2.
ED 01-APR-1999.
XX
PF 14-SEP-1998; 98W0-US019093.
XX
PR 19-SEP-1997; 97US-00933821.
PR 29-OCT-1997; 97US-00960507.
XX
PA (GELT) GENENTECH INC.
XX
PI Godowski PJ, Gurney AL, Hillan K, Botstein D, Goddard A, Roy M;
PI Ferrara N, Tumas D, Schwall R;
XX

DR WP1; 1999-263480/22.
DR N-PSDB; AAX36341.
PT New isolated TIE ligand homologs for, e.g. developing products for
PT treatment of tumors.
XX
XX Claim 8; Fig 3; 132pp; English.
XX
CC This sequence is the human tyrosine kinase containing Ig and EGF homology
CC domains (TIE) ligand of the invention, designated N1.1. The TIE receptors
CC are receptor tyrosine kinases which are expressed in vascular endothelial
CC cells and early haemopoietic cells. The TIE receptors are believed to be
CC actively involved in angiogenesis, and may play a role in haemopoiesis as
CC well. The TIE ligand homologs can promote the survival and/or growth
CC and/or differentiation of TIE receptor expressing cells. They can be used
CC for promoting neovascularisation in wound healing and for promoting
CC angiogenic processes, such as for inducing collateral vascularisation in
CC an ischaemic heart or limb, or for promoting bone development and/or
CC maturation and/or growth in a patient or muscle growth and development.
CC The TIE ligand homologs and antibodies can inhibit the growth of
CC endothelial cells and induce apoptosis of cells, particularly tumour
CC cells. They can inhibit vasculogenesis, particularly the vascularisation
CC of tumour cells. The antibodies can also inhibit vascularisation of a
CC cell in which a gene encoding an N1.1, N1.5, N1.8 or N1.4 polypeptide is
CC amplified. The products can also be used for detection, diagnosis, drug
CC screening and production of transgenic animals
XX
SQ Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 2; Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAAMGAVAGQEDGEGTEGSGRREFTYLRKRAESQDKCTYFTIV 60
DB 1 MRPLCTCWMGLGLAAMGAVAGQEDGEGTEGSGRREFTYLRKRAESQDKCTYFTIV 60
QY 61 POORVTGATCVNSKEPEVLENRVHKQELINNELNKKQKQIETLQQLVADGIVSEV 120
DB 61 POORVTGATCVNSKEPEVLENRVHKQELINNELNKKQKQIETLQQLVADGIVSEV 120
QY 121 KILRKESRMNSRVTLQVWQLHETIRKRDNALBESQLENRIINQTAQMLQASKYKOLE 180
DB 121 KILRKESRMNSRVTLQVWQLHETIRKRDNALBESQLENRIINQTAQMLQASKYKOLE 180
QY 181 HKYQHLATLANHQSSEIIAQLEBHCQVPSARVPQPPAAPPVRYQPTYNRIINQISTN 240
DB 181 HKYQHLATLANHQSSEIIAQLEBHCQVPSARVPQPPAAPPVRYQPTYNRIINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMTLTSLSSTDKSPGPRDCLQALBDGHTSSIYLVKPEPTN 300
DB 241 EIQSDQNLKVLPPPLPTMTLTSLSSTDKSPGPRDCLQALBDGHTSSIYLVKPEPTN 300
QY 301 RLMQVWCDQRHDPGGMVTYIQRLDGSVNFPRWMEYKQGFNIDGEMWLGLENIYWLTNQ 360
DB 301 RLMQVWCDQRHDPGGMVTYIQRLDGSVNFPRWMEYKQGFNIDGEMWLGLENIYWLTNQ 360
QY 361 GNYKLLVTEWDSGKRVFAEYASFRLPESESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLLVTEWDSGKRVFAEYASFRLPESESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAHYQKGGWYNAKAHNSLNGWYRGHRSRYQDGVYAAEFRGSGYSLSKK 480
DB 421 RDHDVYTGNCAHYQKGGWYNAKAHNSLNGWYRGHRSRYQDGVYAAEFRGSGYSLSKK 480
QY 481 VVMIRPNPNTFH 493
DB 481 VVMIRPNPNTFH 493

RESULT 3
AAV54999
ID AAV54999 standard; protein; 493 AA.

XX	AAV54999;
AC	
XX	18-FEB-2000 (first entry)
DT	
XX	Human scarface 1 protein sequence.
XX	
KM	Scarface 1; human; Sf-1 protein; angiogenesis; wound healing; diagnosis;
KW	tumour growth; cancer; stem cell amplification; endothelial cell;
KW	TIE receptor; neoplastic disease; wound healing; thromboembolic disease;
KM	atherosclerosis; inflammatory disease; neovascularisation; ischaemia;
KM	therapy.
XX	
OS	Homo sapiens.
XX	
PN	EP962530-A2.
XX	
PD	08-DEC-1999.
XX	
PF	01-JUN-1999; 9SEP-00304239.
XX	
PR	02-JUN-1998; 9BUS-0087710P.
PR	08-JUN-1998; 9BUS-0088503P.
PR	17-SEP-1998; 9BUS-0100857P.
XX	
PA	(ELIL) LILLY & CO ELI.
P1	Heuer JG, Burgett SG, Leonard RA, Rosteck PR, Sankhavaram PR;
XX	
DR	WPI; 2000-025636/03.
XX	
DR	N-PsDB; AA240049.
PT	New substantially pure Scarface 1 (Sf-1) protein, useful for screening
PT	compounds for modulating angiogenesis, to enhance wound healing, inhibit
PT	tumor growth and/or to amplify stem cells.
PS	Claim 2; Page 20-22; 25pp; English.
XX	
CC	This sequence represents the human Scarface 1 (Sf-1) protein of the
CC	invention. The Sf-1 nucleic acids are useful as probes to isolate
CC	paralogous genes from humans and/or orthologous genes from other
CC	organisms. Sf-1 proteins are also useful to screen for compounds that
CC	bind the peptides as potential pharmaceutical compounds for modulating
CC	angiogenesis. The proteins are useful as therapeutics to enhance wound
CC	healing, for developing compounds for inhibiting tumour growth, for
CC	treating cancer and for use in a method to amplify stem cells. Sf-1
CC	proteins may be further used in the diagnosis and treatment of certain
CC	diseases involving endothelial cells and associated TIE receptors e.g.
CC	neoplastic diseases involving tumour angiogenesis, thromboembolic
CC	diseases, atherosclerosis and inflammatory diseases. In addition the
CC	mammalian ligand may be used to promote proliferation and/or
CC	differentiation of haematopoietic stem cells. Sf-1 may be used to promote
CC	the growth, survival, migration and/or differentiation and/or
CC	stabilisation or destabilisation of cells expressing the receptor.
CC	Biologically active Sf-1 may be used in the in vitro maintenance of the
CC	TIE receptor expressing cells in culture. Alternatively Sf-1 may be used
CC	to support cells which are engineered to express TIE receptor and its
CC	cognate receptor may be used in assay systems to identify (ant.)agonists
CC	of the TIE receptor. Sf-1 may be administered to promote
CC	neovascularisation and especially to treat ischaemia
SQ	
	Sequence 493 AA;
Query Match	99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity	99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative	1; Mismatches 0; Indels 0; Gaps 0
Oy	1 MRRLCTCWWLGLAAMGAVAQGDEGEETEGSSPREFIYLNRYKRGESODKCTYTTFIV 60
Dd	1 MRPLCTCWWLGLAAMGAVAQGDEGEETEGSSPREFIYLNRYKRGESODKCTYTTFIV 60
Oy	60
Dd	60
Oy	120

ID	AA	Protein	Location/Qualifiers
Db	61	PQQRVIGAI.CVNSKEPEVLLERVAHKQELIUNNELLKQKQRIETTLQQLVEVDGIVSEV	
Qy	121	KLIRKESRNNASRVTOIYMQLIHEIIRGRDVALSELQLENRIINQTRADMQLASKYKDE	180
Db	121	KLIRKESRNNASRVTOIYMQLIHEIIRGRDVALSELQLENRIINQTRADMQLASKYKDE	180
Qy	181	HKYQHLATLAHNOSEIIAQLEHCGRVSAFVQPPAPAFRVYQOPPTYNRIINQISTN	240
Db	181	HKYQHLATLAHNOSEIIAQLEHCGRVSAFVQPPAPAFRVYQOPPTYNRIINQISTN	240
Qy	241	EIOSDONLKVLPPEPTPTLTSPSSYDKXSGPWRDCLQALEDHGDTSSIYVVKPENTN	300
Db	241	EIOSDONLKVLPPEPTPTLTSPSSYDKXSGPWRDCLQALEDHGDTSSIYVVKPENTN	300
Qy	301	RLMQWCDQGRHPGGMTYQIRLSDSVAFPPNFMETTYQGFENIDGFWLGLENIYWLINQ	360
Db	301	RLMQWCDQGRHPGGMTYQIRLSDSVAFPPNFMETTYQGFENIDGFWLGLENIYWLINQ	360
Qy	361	GNFKLVLTMEWDSGRKVFALVAFSPLEPESEYVYKLRLGRVHGNAGDSFTWHNGKQFTLLD	420
Db	361	GNFKLVLTMEWDSGRKVFALVAFSPLEPESEYVYKLRLGRVHGNAGDSFTWHNGKQFTLLD	420
Qy	421	RHDVYVTCGAHYQKQGMWYTNCAHSNINQWYVRCGHRTSYQCGYVMAEPFGGSYSLKK	480
Db	421	RHDVYVTCGAHAHQKQGMWYTNCAHSNINQWYVRCGHRTSYQCGYVMAEPFGGSYSLKK	480
Qy	481	VWMMIRPNPNTFH 493	
Db	481	VWMMIRPNPNTFH 493	
RESULT 4			
ID	AA	AA70745	standard; protein; 493 AA.
XX	XX	AA70745;	
AC	XX	24-JUL-2000	(first entry)
DT	XX	PSHQ-3	protein encoded by NSEQ gene associated with matrix remodelling.
DE	XX	NSEQ	gene; matrix-remodelling gene; Incyte clone 2268890; cancer;
XX	XX	NSEQ	matrix-remodelling disease; cardiomyopathy; arthritis; angiogenesis;
KW	KW	diabetic	necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;
KM	KM	cardioactive;	antiarrhythmic; angiogenic; antiarteriosclerotic; antiulcer.
XX	XX	Homo sapiens.	
OS	XX		
XX	XX	Key	Location/Qualifiers
FH	FH	Peptide	1..22
FT	FT	Modified-site	/label= "Signal_peptide"
FT	FT	Modified-site	12
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	18
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	22
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	29
FT	FT	Modified-site	/note= "N-myristoylation site"
FT	FT	Modified-site	34
FT	FT	Modified-site	/note= "Protein kinase C phosphorylation site"
FT	FT	Modified-site	34
FT	FT	Modified-site	/note= "Casein kinase II phosphorylation site"
FT	FT	Modified-site	127
FT	FT	Modified-site	/note= "cAMP- and cGMP-dependent protein kinase"
FT	FT	Modified-site	164
FT	FT	Modified-site	/note= "N-glycosylation site"
FT	FT	Modified-site	183
FT	FT	Modified-site	/note= "Tyrosine kinase phosphorylation site"
FT	FT	Modified-site	192
FT	FT	Modified-site	/note= "N-glycosylation site"
FT	FT	Modified-site	209
FT	FT	Modified-site	/note= "Protein kinase C phosphorylation site"

PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
XX
XX
XX (GENETECH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
PI Godowski PJ, Gueney AL, Kijavitt J, Napier MA, Pan J,
PI Paoni NF, Roy MA, Stewart TA, Tamas D, Watanabe CK, Williams PM,
PI Wood WI, Zhang Z;
XX
XX MPI: 2001-050091/06.
DR N-PSDB; AAC86961.

PT Isolated nucleic acid molecule encoding a pro polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides.

XX Claim 12; Fig 2; 24pp; English.

XX The present sequence represents a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO419, PRO499, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO33, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO1096, PRO603,
CC PRO604, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene
XX
XX

Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 4; Length 493;

Best Local Similarity 99.8%; Pred. No. 1,4e-216;

Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRPVLTGAI CVNSKEPEVLLNRRVHKOLELNNLLKOKQIETLQQLVVDGIVSEV 60
DB 1 KRPVLTGAI CVNSKEPEVLLNRRVHKOLELNNLLKOKQIETLQQLVVDGIVSEV 60
QY 61 PQRVTGAI CVNSKEPEVLLNRRVHKOLELNNLLKOKQIETLQQLVVDGIVSEV 120
DB 61 PQRVTGAI CVNSKEPEVLLNRRVHKOLELNNLLKOKQIETLQQLVVDGIVSEV 120
QY 121 KLRKESNNMSRVTLQMLHETIRKDNALISOLENLIQOTADMLQASKYDLE 180
DB 121 KLRKESNNMSRVTLQMLHETIRKDNALISOLENLIQOTADMLQASKYDLE 180
QY 181 HKYQIATLANOSEIILAEHEHCQVPSARVPPOPPAPPRVYQPTVYRIINOISTN 240
DB 181 HKYQIATLANOSEIILAEHEHCQVPSARVPPOPPAPPRVYQPTVYRIINOISTN 240
QY 241 EIQSNNKLVPPPTPTLTLSPSSTDKPSGPRDQLQLEGHGHTSSYLVKPEPNTN 300
DB 241 EIQSNNKLVPPPTPTLTLSPSSTDKPSGPRDQLQLEGHGHTSSYLVKPEPNTN 300
QY 301 RLMQVCDQRHDPGSGMTVIOIRLDGSVNFNNMETYKQGFNDIGEWLGLNIIYWLNQ 360
DB 301 RLMQVCDQRHDPGSGMTVIOIRLDGSVNFNNMETYKQGFNDIGEWLGLNIIYWLNQ 360
QY 361 GNYKLVVMEWWSGKVAFAEYASFLLEPESYIKLRIGRYHGNAGDSFTWNGQFTLLD 420
DB 361 GNYKLVVMEWWSGKVAFAEYASFLLEPESYIKLRIGRYHGNAGDSFTWNGQFTLLD 420
QY 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGWYRGHRSRYQGYVMAEFRRGSYSLLKK 480
DB 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGWYRGHRSRYQGYVMAEFRRGSYSLLKK 480

DB 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGWYRGHRSRYQGYVMAEFRRGSYSLLKK 480
QY 481 VMMAIRPENTFH 493
DB 481 VMMAIRPENTFH 493

RESULT 7
ID AAU12305
AAU12305 standard; protein; 493 AA.

XX AAU12305;

XX 24-OCT-2001 (first entry)

XX Human PRO196 polypeptide sequence.

XX Human secretory and transmembrane; PRO, mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIa; gene therapy.

XX Homo sapiens.

XX WO200140466-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US032678.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 11-FEB-2000; 2000WO-US000376.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004342.

XX 24-FEB-2000; 2000WO-US004914.

XX 24-FEB-2000; 2000WO-US005004.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-018702P.

XX 10-MAR-2000; 2000WO-US006319.

XX 15-MAR-2000; 2000WO-US006884.

XX 20-MAR-2000; 2000WO-US007377.

XX 21-MAR-2000; 2000WO-US007532.

XX 30-MAR-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

XX 22-MAY-2000; 2000WO-US014042.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 28-JUL-2000; 2000WO-US020710.

XX 11-AUG-2000; 2000WO-US022031.

XX 23-AUG-2000; 2000WO-US023523.

XX 24-AUG-2000; 2000WO-US023328.

XX 08-NOV-2000; 2000WO-US030952.

XX 10-NOV-2000; 2000WO-US030875.

(GENETECH) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerltsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21377.
XX
XX
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
PS
PS Claim 12; Fig 268; 813pp; English.

AAU2172-AAU2446 represent novel human secretory and transmembrane PRO
polypeptides. The PRO polypeptides are useful to detect other PRO
polypeptides, to link bioactive molecules to cells expressing PRO
polypeptides, to modulate biological activities of cells expressing PRO
polypeptides, and to detect the presence of mammalian lung, colon,
breast, prostate, rectal, cervical or liver tumors by comparing PRO
polypeptide expression in a cell sample to that in a control sample. Some
of the 275 sequences are also useful to stimulate the release of tumour
necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
differentiation of chondrocytes, the proliferation or gene expression in
pericyte cells, the release of proteoglycans from cartilage, the
proliferation of inner ear utricular supporting cells or of T-
lymphocytes, the release of a cytokine from peripheral blood monocytes
(PBMCs), or the proliferation of endothelial cells. Some of the PRO
polypeptides may modulate glucose or free fatty acid uptake by skeletal
muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
VIIa. The PRO polypeptides can be used in assays to identify molecules
involved in binding interactions. The polynucleotides encoding PRO
polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy

Sequence 493 AA:

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMVGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
DB 1 MRPLCTCWMVGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
QY 61 PQRVTGALCVNSKEPEVLLNRYKHQKLELNNELKQKQIETLQQLVYDGGIVSEV 120
DB 61 PQRVTGALCVNSKEPEVLLNRYKHQKLELNNELKQKQIETLQQLVYDGGIVSEV 120
QY 121 KLLKRESRMNSRYTQLYMQLHEIIRKDNALLESQLENRIINQTDMLQLASKYKDL 180
DB 121 KLLKRESRMNSRYTQLYMQLHEIIRKDNALLESQLENRIINQTDMLQLASKYKDL 180
QY 181 HKYQHLATLANQSEIIAQLSEHCQVPSARVPVOPPPAPRVYQPTVNRINQISTN 240
DB 181 HKYQHLATLANQSEIIAQLSEHCQVPSARVPVOPPPAPRVYQPTVNRINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGWRDCLQALEDHGHTSSITLVKPENTN 300
DB 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGWRDCLQALEDHGHTSSITLVKPENTN 300
QY 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFPRMWTYKQGFNIDEXYMLGLENITWLTNQ 360
DB 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFPRMWTYKQGFNIDEXYMLGLENITWLTNQ 360
QY 361 GNYKLLVTMEWDSGRKVFAYASFRLEPSEYYKLRIGYHGNAGDSFTWANGKQFTTLD 420
DB 361 GNYKLLVTMEWDSGRKVFAYASFRLEPSEYYKLRIGYHGNAGDSFTWANGKQFTTLD 420
QY 421 RHDHVTYTGCAHYOKGGMWYNACAHSNLNGVYRGGHVSRYODGVYMAFFGGSYSLLK 480
DB 421 RHDHVTYTGCAHYOKGGMWYNACAHSNLNGVYRGGHVSRYODGVYMAFFGGSYSLLK 480
QY 481 VVMIMIRNPNTFH 493

DB 481 VVMIMIRNPNTFH 493

RESULT 8
AAB51329
ID AAB51329 standard; protein; 493 AA.

AC AAB51329;

XX 02-APR-2001 (first entry)

XX Human 410 angiotensin-like protein SEQ ID NO:4.

XX Human; 410; NEW; angiotensin-like protein; angiotensin.

XX Homo sapiens.

XX JP2000300263-A.

XX 31-OCT-2000.

XX 14-APR-1999; 99JP-00107234.

XX 14-APR-1999; 99JP-00107234.

XX (HERI-) HERIKUSU KENYUSHO KK.

XX WPI; 2001-151128/16.

XX N-PSDB; AAF26789.

PT New genes encoding angiotensin-like proteins 410 and NEW, useful for the
PT prevention and treatment of diseases relating to angiotensin.

PS Claim 1; Page 12-13; 26pp; Japanese.

CC The present invention describes two human angiotensin-like proteins
CC designated 410 and NEW. The angiotensin-like proteins can be used for
CC the prevention and treatment of diseases relating to angiotensin. The
CC present sequence represents the human 410 angiotensin-like protein.

Sequence 493 AA:

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMVGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
DB 1 MRPLCTCWMVGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
QY 61 PQRVTGALCVNSKEPEVLLNRYKHQKLELNNELKQKQIETLQQLVYDGGIVSEV 120
DB 61 PQRVTGALCVNSKEPEVLLNRYKHQKLELNNELKQKQIETLQQLVYDGGIVSEV 120
QY 121 KLLKRESRMNSRYTQLYMQLHEIIRKDNALLESQLENRIINQTDMLQLASKYKDL 180
DB 121 KLLKRESRMNSRYTQLYMQLHEIIRKDNALLESQLENRIINQTDMLQLASKYKDL 180
QY 181 HKYQHLATLANQSEIIAQLSEHCQVPSARVPVOPPPAPRVYQPTVNRINQISTN 240
DB 181 HKYQHLATLANQSEIIAQLSEHCQVPSARVPVOPPPAPRVYQPTVNRINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGWRDCLQALEDHGHTSSITLVKPENTN 300
DB 241 EIQSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGWRDCLQALEDHGHTSSITLVKPENTN 300
QY 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFPRMWTYKQGFNIDEXYMLGLENITWLTNQ 360
DB 301 RLMQVWCDQRHDPGGWTVIQRRLDGSVNFPRMWTYKQGFNIDEXYMLGLENITWLTNQ 360
QY 361 GNYKLLVTMEWDSGRKVFAYASFRLEPSEYYKLRIGYHGNAGDSFTWANGKQFTTLD 420
DB 361 GNYKLLVTMEWDSGRKVFAYASFRLEPSEYYKLRIGYHGNAGDSFTWANGKQFTTLD 420

```
DB 361 GNYKLLVTMEDWSGRKVPFAEYASFRLEPSEYYKTLGRYHGNAGDSFTWHNGKQFTILD 420
QY 421 RDHDVYTGCAHYOKGGMWYNACAHSNLNGVWYRGHYSRYODGVYMAEPRGGSYSLLKX 480
DB 421 RDHDVYTGCAHYOKGGMWYNACAHSNLNGVWYRGHYSRYODGVYMAEPRGGSYSLLKX 480
QY 481 VVMMIRPNPTFH 493
DB 481 VVMMIRPNPTFH 493

RESULT 9
AA014786
ID AA014786 standard; protein; 493 AA.
XX
AC AA014786;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human matrix-remodeling-associated protein 3.
XX
KM Human; matrix-remodeling gene; extracellular matrix;
KM matrix-remodeling-associated nucleotide; screening;
KM matrix-remodeling-associated disease; angiogenesis; arthritis;
KM atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;
KM ulceration.
XX
OS Homo sapiens.
XX
PN US2002019000-A1.
XX
PD 14-FEB-2002.
XX
PF 26-MAR-2001; 2001US-00818143.
XX
PR 09-OCT-1998; 98US-00169289.
XX
PA (WALK/) WALKER M G.
PA (VOLK/) VOLKUTH W.
PA (KLIN/) KLINGLER T M.
PI Walker MG, Volkuth W, Klingler TM;
DR WPI; 2002-338319/37.
DR N-PSDB; AAL42455.
XX
PT New isolated polynucleotide coexpressed with matrix-remodeling genes,
PT useful in diagnosis, prognosis, prevention and treatment of diseases
PT associated with matrix-remodeling such as angiogenesis, arthritis and
PT cancer.
XX
PS Example; Fig 3; 63pp; English.
XX
CC The invention comprises human nucleotide sequences which are co-expressed
CC with matrix-remodeling genes. Matrix-remodeling is associated with the
CC construction, destruction and reorganisation of extracellular matrix
CC components. The matrix-remodeling-associated nucleotides of the invention
CC are useful for screening for and purifying ligands that specifically bind
CC to the nucleotides of the invention. The matrix-remodeling-associated
CC nucleotides of the invention are also useful in the diagnosis, prognosis,
CC prevention, treatment and evaluation of therapies for diseases associated
CC with matrix remodeling (e.g. angiogenesis, arthritis, atherosclerosis,
CC cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The
CC present amino acid sequence is encoded by a human matrix-remodeling-
CC associated nucleotide of the invention
XX
SQ Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 5; Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCVTCWMLGLLAAMGAVAGQEDGFECTEGSFRERYINRYKRAGESQDKCTYTFIV 60
```

```
DB 1 MRPLCVTCWMLGLLAAMGAVAGQEDGFEGBEESPREFIYINRYKRAGESQDKCTYTFIV 60
QY 61 POGRYTGAICVNSKEPEVLLNRYHKOELJLNNELLKQKQETIQOJYKVDGIVSEV 120
DB 61 POGRYTGAICVNSKEPEVLLNRYHKOELJLNNELLKQKQETIQOJYKVDGIVSEV 120
QY 121 KLRKESRRNNNSRVTLQYMLLHEIRKRDNALELSQLENRLINQTAADYLQASKYKDE 180
DB 121 KLRKESRRNNNSRVTLQYMLLHEIRKRDNALELSQLENRLINQTAADYLQASKYKDE 180
QY 181 HKYQHATTAHNSSEIIAQLEEHQVPSARPYPPPPAPPRVYQPPYNNIINOISYN 240
DB 181 HKYQHATTAHNSSEIIAQLEEHQVPSARPYPPPPAPPRVYQPPYNNIINOISYN 240
QY 241 EIOSDQYLKVLPEPLPTMPLTSLPSTPKPSGPFMRDCQALEDHDTSSILVKEPENT 300
DB 241 EIOSDQYLKVLPEPLPTMPLTSLPSTPKPSGPFMRDCQALEDHDTSSILVKEPENT 300
QY 301 RLMQWCDQHDHDEGWTVIQRIDGSVNFPRMNEYKQGFNIDGFWLGLNITWLNQ 360
DB 301 RLMQWCDQHDHDEGWTVIQRIDGSVNFPRMNEYKQGFNIDGFWLGLNITWLNQ 360
QY 361 GNYKLLVTMEDWSGRKVPFAEYASFRLEPSEYYKTLGRYHGNAGDSFTWHNGKQFTILD 420
DB 361 GNYKLLVTMEDWSGRKVPFAEYASFRLEPSEYYKTLGRYHGNAGDSFTWHNGKQFTILD 420
QY 421 RDHDVYTGCAHYOKGGMWYNACAHSNLNGVWYRGHYSRYODGVYMAEPRGGSYSLLKX 480
DB 421 RDHDVYTGCAHYOKGGMWYNACAHSNLNGVWYRGHYSRYODGVYMAEPRGGSYSLLKX 480
QY 481 VVMMIRPNPTFH 493
DB 481 VVMMIRPNPTFH 493

RESULT 10
ABG80355
ID ABG80355 standard; protein; 493 AA.
XX
AC ABG80355;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human TIE ligand NL1 protein.
XX
KM Human; TIE ligand NL4; vascularisation; wound healing; heart; limb;
KM ischemic condition; vulnerability; vasotropic; gene therapy; NL1; NL5; NL8.
XX
OS Homo sapiens.
XX
PN US6413770-B1.
XX
PD 02-JUL-2002.
XX
PF 19-AUG-1998; 98US-00136801.
XX
PR 19-SEP-1997; 97US-00933821.
PR 29-OCT-1997; 97US-00960507.
XX
PA (GETH ) GENENTECH INC.
PA Godowski P, Gurney A, Hillan KJ, Botstein D, Goddard A, Roy M;
PI Ferrara N, Tumas D, Schwall R;
XX
DR WPI; 2002-641562/69.
DR N-PSDB; ABS65529.
XX
PT Novel isolated nucleic acid molecules encoding NL4 TIE ligand homologue
PT polypeptides which are useful for inducing vascularization for wound
PT healing and treating ischemic condition of the heart or a limb.
XX
PS Example 1; Fig 3; 85pp; English.
```

XX The present invention relates to a new nucleic acid molecule which
 CC comprises nucleotides 215 to 1252 of fully defined T1E ligand N14
 CC polynucleotide sequence of 2212 base pairs as given in the specification.
 CC The nucleic acid of the invention encodes N14 T1E ligand homologue
 CC polypeptide. The invention is useful for expressing N14 T1E ligand
 CC homologue polypeptide by recombinant techniques. T1E ligand homologue
 CC polypeptide is useful for inducing vascularisation for promoting wound
 CC healing and for treating ischemic condition of heart or limb. The
 CC present amino acid sequence represents a human T1E ligand protein, as
 CC described in the invention

XX Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 5; Length 493;

Best Local Similarity 99.8%; Pred. No. 1,4e-216; Mismatches 0; Indels 0; Gaps 0;

Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MRPLCTCMTGILAMGAVAGQEDGEGTEGSPREFIYNRYKRGESQDKCTYTFIV 60
 1 MRPLCTCMTGILAMGAVAGQEDGEGTEGSPREFIYNRYKRGESQDKCTYTFIV 60
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480
 481 VVMATIRPNNTFH 493
 481 VVMATIRPNNTFH 493
 481 VVMATIRPNNTFH 493

RESULT 11

ID AAE19825 standard; protein; 493 AA.

XX AAE19825;

18-JUN-2002 (first entry)

Human T1E ligand N14 protein.

Human; T1E ligand; N14; cytosolic; osteopathic; vascularisation; toxin;

muscular; immunosassay; therapeutic; anti-tumour agent; muscle growth;

bone development; maturation; angiogenesis.

Homo sapiens.

US6350450-B1.

PD 26-FEB-2002.

PF 19-AUG-1998; 98US-00136828.

FR 19-SEP-1997; 97US-0059588P.

PA (GETH) GENENTECH INC.

PI Goddard PJ, Gurney AL, Goddard A, Hillan K;

DR WPI; 2002-215264/27.

DR N-PSDB; AAD31563.

PT Novel isolated antibody which specifically binds to a mammalian N14 T1E
 PT ligand useful for immunoassays, delivery of cytotoxic molecules and as
 PT diagnostic agents to detect disease states.

PS Claim 1; Fig 3; 59pp; English.

XX The invention relates to an isolated antibody which specifically binds to
 CC a mammalian N14 T1E (tyrosine kinase containing Ig and EGF homology
 CC domains) ligand polypeptide which is capable of inducing vascularisation.
 CC The isolated antibody may be used in immunoassays to measure the amount
 CC of a T1E ligand in a biological sample. Additionally, the antibody may be
 CC used for the delivery of cytotoxic molecules, e.g. radioisotopes or
 CC toxins, or therapeutic agents to cells expressing a corresponding T1E
 CC receptor. The therapeutic agents may, for example, be other T1E ligands,
 CC including the T1E-2 ligand, members of the vascular endothelial growth
 CC factor (VEGF) family, or known anti-tumour agents, and agents known to be
 CC associated with muscle growth or development, or bone development.
 CC maturation, or growth. Anti-T1E ligand antibodies are also suitable as
 CC diagnostic agents, to detect disease states associated with the
 CC expression of a T1E (e.g. T1E-2) receptor. These detectably labelled
 CC antibody agonists of a T1E receptor can be used for imaging the presence
 CC of angiogenesis. The present sequence is human T1E ligand N14 protein
 XX Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 5; Length 493;

Best Local Similarity 99.8%; Pred. No. 1,4e-216; Mismatches 0; Indels 0; Gaps 0;

Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MRPLCTCMTGILAMGAVAGQEDGEGTEGSPREFIYNRYKRGESQDKCTYTFIV 60
 1 MRPLCTCMTGILAMGAVAGQEDGEGTEGSPREFIYNRYKRGESQDKCTYTFIV 60
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 61 PQRRTGAI CVNSKEPEVLL ENRVKQEL LNELLKOKQIETLQQLVVDGIVSEV 120
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 121 KLRKESRNMNSRVTOLYQMLHEIIRKDNAL ELSOLENRLINQTDMLQASKYKXDL 180
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 181 HKYQHLATLANQSEIIAQL EHCQVPSARVPVPPAPPRVYQPTNRIINQISTN 240
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 241 EIQSDONLKVLPPLPMTPTLSLPSSTDKPSGPRDCIQLALEDGHTSSIVLVKPEPTN 300
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 301 RLMQVCDQRHDPGQMTVIO RRLDGSVNFERNWETTKQFGNIDGEYWLGENIYWLTNQ 360
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 361 GNYKLLVTMEDMSGRKFAEYASFRLEPSEYYKRLRGYHGNAGDSFTMHNGKQFTLLD 420
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480
 421 RDHDVYTGNCAYHKGGMWYNACAHSNLNGVWYRGHYRSRYQDGVYAAEFRGGSYSLLK 480

Qy	481	VMMTRPNTPEH	493
Db	481	VMMTRPNTPEH	493
RESULT 12			
ABOI7749			
ID	ABOI7749	standard; protein; 493 AA.	
XX			
AC	ABOI7749;		
XX			
DT	26-AUG-2003	(first entry)	
XX			
DE	Novel human secreted and transmembrane protein PRO196.		
XX			
KW	Human; secreted and transmembrane protein; PRO: antiinflammatory;		
KW	antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;		
KW	TNF-alpha release; cell proliferation; cell differentiation;		
KW	gene expression modulator; proteoglycan release; cytokine release;		
KW	tumour; inflammatory disease; organ failure; atherosclerosis;		
KW	cardiac injury; infertility; birth defect; premature aging; AIDS;		
KW	acquired immunodeficiency syndrome; cancer; diabetic complication;		
KW	chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor		
XX	bioreactor; tissue typing.		
XX			
OS	Homo sapiens.		
XX			
PN	US2003032156-A1.		
XX			
PD	13-FEB-2003.		
XX			
PF	06-MAY-2002; 2002US-00140474.		
XX			
PR	31-MAR-1997; 97WO-US005230.		
PR	12-JUN-1998; 98WO-US012456.		
PR	14-JUL-1998; 98WO-US014552.		
PR	28-AUG-1998; 98WO-US017688.		
PR	10-SEP-1998; 98WO-US018682.		
PR	14-SEP-1998; 98WO-US019093.		
PR	14-SEP-1998; 98WO-US019094.		
PR	14-SEP-1998; 98WO-US019177.		
PR	16-SEP-1998; 98WO-US019330.		
PR	17-SEP-1998; 98WO-US019437.		
PR	07-OCT-1998; 98WO-US021141.		
PR	29-OCT-1998; 98WO-US022991.		
PR	29-OCT-1998; 98WO-US022992.		
PR	20-NOV-1998; 98WO-US024835.		
PR	01-DEC-1998; 98WO-US025108.		
PR	05-JAN-1999; 99WO-US000106.		
PR	08-MAR-1999; 99WO-US005028.		
PR	10-MAR-1999; 99WO-US005190.		
PR	20-APR-1999; 99WO-US008615.		
PR	14-MAY-1999; 99WO-US010733.		
PR	02-JUN-1999; 99WO-US012252.		
PR	01-SEP-1999; 99WO-US020111.		
PR	08-SEP-1999; 99WO-US020594.		
PR	13-SEP-1999; 99WO-US020944.		
PR	15-SEP-1999; 99WO-US021090.		
PR	15-SEP-1999; 99WO-US021547.		
PR	05-OCT-1999; 99WO-US023069.		
PR	29-NOV-1999; 99WO-US028214.		
PR	30-NOV-1999; 99WO-US028313.		
PR	30-NOV-1999; 99WO-US028401.		
PR	01-DEC-1999; 99WO-US028301.		
PR	01-DEC-1999; 99WO-US028634.		
PR	02-DEC-1999; 99WO-US028651.		
PR	02-DEC-1999; 99WO-US028654.		
PR	16-DEC-1999; 99WO-US028655.		
PR	16-DEC-1999; 99WO-US030095.		
PR	20-DEC-1999; 99WO-US030911.		
PR	20-DEC-1999; 99WO-US030999.		

PT infertility, birth defects, premature aging, acquired immunodeficiency
XX syndrome (AIDS), or cancer.
XX Claim 12; Fig 268; 660pp; English.
XX The invention describes an isolated nucleic acid (1) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (1) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIa, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 6; Length 493;
Best Local Similarity 99.8%; Pred. No. 1.4e-216;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVTCWMLGLLAMGAVAGQEDFGTEGSGREFIYLNRYRAESQDKCYTIV 60
DB 1 MRPLVTCWMLGLLAMGAVAGQEDFGTEGSGREFIYLNRYRAESQDKCYTIV 60
QY 61 POORVTGACVNSKEPEVLLNRYVHKOELIENLNLKQKQIETLOOLVYVGGIVSEV 120
DB 61 POORVTGACVNSKEPEVLLNRYVHKOELIENLNLKQKQIETLOOLVYVGGIVSEV 120
QY 121 KLLRRESRNMSRVTLQVLIHEIIRKDNALIEQLBNRLNQTADMLQASRYKOLE 180
DB 121 KLLRRESRNMSRVTLQVLIHEIIRKDNALIEQLBNRLNQTADMLQASRYKOLE 180
QY 181 HYYCHLATLHNSQELIAGLEHCORVPSARVPOPPAPPRVYQPTVRIINQISTN 240
DB 181 HYYCHLATLHNSQELIAGLEHCORVPSARVPOPPAPPRVYQPTVRIINQISTN 240
QY 241 EIISDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPRDCIQALEDHSTISYLVKPENTN 300
DB 241 EIISDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPRDCIQALEDHSTISYLVKPENTN 300
QY 301 RLMQWMCORHDPGCMTVIGRLDGSVNFERNWETVYKQFGNIDDEYVLGENTVWLTNO 360
DB 301 RLMQWMCORHDPGCMTVIGRLDGSVNFERNWETVYKQFGNIDDEYVLGENTVWLTNO 360
QY 361 GNYKLLVTWEDWSGKRVFAEYASFLPEPESEYKRLGRYHGNAGDSFTWNGKQFTILD 420
DB 361 GNYKLLVTWEDWSGKRVFAEYASFLPEPESEYKRLGRYHGNAGDSFTWNGKQFTILD 420
QY 421 RHHVYITGCAHYKQGGWYVYNAHNSNLNGVYRGGHYRSRQDGVYAAEPFGSGYSILK 480
DB 421 RHHVYITGCAHYKQGGWYVYNAHNSNLNGVYRGGHYRSRQDGVYAAEPFGSGYSILK 480
QY 481 VMMKIRPNFTFH 493
DB 481 VMMKIRPNFTFH 493

RESULT 13
ABO25150

ID ABO25150 standard; protein; 493 AA.
XX
AC ABO25150;
XX
DT 05-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO196.
XX
KW Human, secreted and transmembrane protein; PRO; antidiabetic;
KW opthalmological; cytostatic; immunostimulant; gene therapy;
KW vascular endothelial growth factor inhibitor; hypertrophy of adult heart;
KW protein secretion disorder; pancreas disorder; diabetes;
KW vascular permeability; retinal neuron cell survival; retinal disorder;
KW immune response; inflammation; mononuclear cell infiltration;
KW eosinophil infiltration; apoptosis; neoplastic growth.
XX
OS Homo sapiens.
XX
PN US2003040014-A1.
XX
PD 27-FEB-2003.
XX
PP 01-FEB-2002; 2002US-00066269.
XX
PR 26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059568P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 25-NOV-1997; 97US-0066684P.
PR 16-DEC-1997; 97US-0069684P.
PR 09-FEB-1998; 98US-0074086P.
PR 09-FEB-1998; 98US-0074092P.
PR 25-MAR-1998; 98US-0079294P.
PR 08-APR-1998; 98US-0081049P.
PR 14-JUL-1998; 98WO-US014852.
PR 10-AUG-1998; 98US-0095985P.
PR 18-AUG-1998; 98US-0097000P.
PR 09-SEP-1998; 98US-0099601P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099811P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 24-SEP-1998; 98US-0101922P.
PR 28-OCT-1998; 98US-0106032P.
PR 20-NOV-1998; 98US-0109304P.
PR 20-NOV-1998; 98WO-US024855.
PR 25-NOV-1998; 98WO-US025190.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US005028.
PR 23-MAR-1999; 99US-0125778P.
PR 02-JUN-1999; 99WO-US012252.
PR 15-JUN-1999; 99US-013695P.
PR 20-JUL-1999; 99US-0145070P.
PR 26-JUL-1999; 99US-0145688P.
PR 17-AUG-1999; 99US-0149396P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
PR 07-DEC-1999; 99US-0169495P.

PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 09-MAR-2000; 2000WO-US006471.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 11-AUG-2000; 2000WO-US022031.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US026728.
 PR 28-FEB-2001; 2001WO-US005520.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 15-NOV-2001; 2001US-00002796.
 XX
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gao W, Garber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Kijavini IJ, Mather JP, Napier MA, Pan J;
 PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
 PI Wood WI, Zhang Z;
 XX
 XX
 DR WPI; 2003-503396/47.
 DR N-PSDB; ACD42312.
 XX
 PT New secreted and transmembrane PRO polypeptides, useful for treating
 PT diabetes, retinal disorders and stimulating an immune response.
 XX
 PS Claim 12; Fig 2; 254pp; English.
 XX
 CC The invention describes an isolated polypeptide (I) having at least 80 %
 CC amino acid sequence identity to 30 secreted and transmembrane
 CC polypeptides. PRO polypeptides are also useful for stimulating
 CC hypertrophy of adult heart, for inhibiting vascular endothelial growth
 CC factor stimulated proliferation of endothelial cells, stimulating
 CC proliferation of stimulated T-lymphocytes and for inducing proliferation
 CC of PD312 pancreatic ductal cells and are thus useful in the treatment of
 CC disorders which involve protein secretion by the pancreas, including
 CC diabetes. PRO polypeptides are useful for inducing vascular permeability
 CC and in enhancing survival of retinal neurons cells and are thus useful
 CC for the treatment of retinal disorders. PRO polypeptides are also useful
 CC for stimulating an immune response and inducing inflammation by inducing
 CC mononuclear cell and eosinophil infiltration at the site of infection of
 CC an animal. The PRO polypeptides are further useful for inducing apoptosis
 CC in endothelial cells for inhibiting neoplastic growth. This is the amino
 CC acid sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 XX
 SQ Sequence 493 AA;
 Query Match 99.9%; Score 2682; DB 6; Length 493;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MRPVLTGWMGLLAAAGVAGQEDGFGTEGSRERITYNRYKRAESODKCTYTFIV 60
 Db 1 MRPVLTGWMGLLAAAGVAGQEDGFGTEGSRERITYNRYKRAESODKCTYTFIV 60
 Oy 61 PQRVTGATCVNSKEPEVLENRVHKQELINNELLKQKQIETLOLVVVDGIVSEV 120
 Db 61 PQRVTGATCVNSKEPEVLENRVHKQELINNELLKQKQIETLOLVVVDGIVSEV 120

Oy 121 KLRKESRNNSRVLTQYLNQQLHEIRKRDNALELSQLENRLINQADMIQLASKYKDE 180
 Db 121 KLRKESRNNSRVLTQYLNQQLHEIRKRDNALELSQLENRLINQADMIQLASKYKDE 180
 Oy 181 HKYQHATTAHNSSEIIIAQLEHCQVPSARPYVPPAPAPRVYQPPYRNRIINQISN 240
 Db 181 HKYQHATTAHNSSEIIIAQLEHCQVPSARPYVPPAPAPRVYQPPYRNRIINQISN 240
 Oy 241 EIOSDONLKVLPPLPLTMTPLTSLPSTDPKPSGPFMDCCQALDEGHDTSIYLKPEENT 300
 Db 241 EIOSDONLKVLPPLPLTMTPLTSLPSTDPKPSGPFMDCCQALDEGHDTSIYLKPEENT 300
 Oy 301 RLMQWCDORHDPGWTVIQRRIDGSVNFPRNNEYKQGFNGIDGHWLGLENIYWLINQ 360
 Db 301 RLMQWCDORHDPGWTVIQRRIDGSVNFPRNNEYKQGFNGIDGHWLGLENIYWLINQ 360
 Oy 361 GNTKLVYTEDWSGRVFAFVAFVAFSEFRLEPSEYKRLGTHGNAGDSFTWNGKQFTTD 420
 Db 361 GNTKLVYTEDWSGRVFAFVAFVAFSEFRLEPSEYKRLGTHGNAGDSFTWNGKQFTTD 420
 Oy 421 RDHDVYTGNCAPHYQKGGWYNACAHSNLNGWYRGSHYRSYQDGVYMAEPRGGSYSLK 480
 Db 421 RDHDVYTGNCAPHYQKGGWYNACAHSNLNGWYRGSHYRSYQDGVYMAEPRGGSYSLK 480
 Oy 481 VVMVIRPNPTFH 493
 Db 481 VVMVIRPNPTFH 493
 RESULT 14
 ADA01417
 ID ADA01417 standard; protein; 493 AA.
 XX
 AC ADA01417;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human angiotensin-related protein 2 SEQ ID NO:20.
 XX
 KM drug testing; hyperlipaemia; arteriosclerosis; hyperglycaemia;
 KM antihypertensive; antihypertensive; antidiabetic; gene therapy; human;
 KM angiotensin-related protein 2.
 XX
 CS Homo sapiens.
 XX
 PN WO2002101039-A1.
 XX
 PD 15-DEC-2002.
 XX
 PF 07-JUN-2002; 2002WO-JP005657.
 XX
 PR 08-JUN-2001; 2001JP-0017758.
 PR 13-JUN-2001; 2001JP-00178548.
 PR 13-JUL-2001; 2001JP-0021334.
 PR 28-SEP-2001; 2001JP-00300715.
 PR 28-SEP-2001; 2001JP-00300716.
 PR 22-NOV-2001; 2001JP-00357037.
 PR 18-DEC-2001; 2001JP-00384103.
 PR 05-APR-2002; 2002JP-00103583.
 XX
 XX
 PA (SANTY) SANTO CO LTD.
 XX
 XX
 PI Koishi R, Ando Y, Ono M, Yasuno H, Shimizuigawa T, Yoshida K;
 PI Shimamura M, Furukawa H;
 XX
 DR WPI; 2003-148803/14.
 DR N-PSDB; ADA01416.
 XX
 PT Testing drugs to treat or prevent diseases e.g. hyperlipaemia,
 PT arteriosclerosis and hyperglycaemia by culturing with transformant cells
 PT then detecting e.g. decrease in mRNA expression dose.
 XX

PS Claim 25; Page 235-237; 279pp; Japanese.

CC The present invention describes a method for testing drugs that have
CC actively on treating or preventing at least 1 disease selected from
CC hyperlipaemia, arteriosclerosis and hyperglycaemia, which comprises
CC culturing cells originating from a mammal in the presence or absence of a
CC test substance, and detecting expression dose of the mRNA with any of the
CC specified nucleotide sequences. More specifically the method comprises:
CC (a) culturing cells originating from a mammal in the presence or absence
CC of a test substance; (b) detecting expression dose of the mRNA with any
CC of the nucleotide sequences (i)-(v) (where c and u are exchangeable); (i)
CC nucleotides 47-1411 of a 1604 base pair sequence (ADA01398); (ii)
CC nucleotides 78-1457 of a 1716 base pair sequence (ADA01400); (iii) the
CC DNA inserted with a phagemid sustaining in the transformant E. coli
CC PBK/m55-1 SANK 72199 (FERM BP-6940); (iv) the DNA inserted with a
CC phagemid sustaining in the transformant E. coli pTrit/h55-1 SANK 72299
CC (FERM BP-6941); or (v) a nucleotide sequence hybridisable with a
CC polynucleotide containing the antisense sequence of (i)-(iv) under
CC stringent conditions and encoding a polypeptide with the activity of
CC increasing neutral lipid concentration in serum; and (c) comparing the
CC resultant expression doses for selecting a test substance. The nucleotide
CC sequences (i)-(v) have antihyperglycaemic, antihyperlipaemic and
CC antidiabetic activities, and can be used in gene therapy. The method is
CC for testing drugs to treat or prevent diseases e.g. hyperlipaemia,
CC arteriosclerosis and hyperglycaemia. The present sequence is used in the
CC exemplification of the present invention.

CC Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 6; Length 493;
Best Local Similarity 99.8%; Pred.No. 1,4e-216; Indels 0; Gaps 0;
Matches 492; Conservative 1; Mismatches 0;

QY 1 MRPLCVTGMWGLLAAAGVAGQEDGEGTEGSPREFIYINRYKAGESQDKTYTIV 60
DB 1 MRPLCVTGMWGLLAAAGVAGQEDGEGTEGSPREFIYINRYKAGESQDKTYTIV 60
QY 61 POORVTGAI CVNSKEPEVILENRYKQLEILNNELNOKQOIEFLQOLVYKDGIVSEV 120
DB 61 POORVTGAI CVNSKEPEVILENRYKQLEILNNELNOKQOIEFLQOLVYKDGIVSEV 120
QY 121 KILRESRNMSRVQLVWQOLHEIIRKDNALLESQJENILNONTAQLASRYKOLE 180
DB 121 KILRESRNMSRVQLVWQOLHEIIRKDNALLESQJENILNONTAQLASRYKOLE 180
QY 181 HKYQHLATLANQSEIIIAQLBEHCQVPSARVPQPPAPAPRYVQPTVNRRIINQISTN 240
DB 181 HKYQHLATLANQSEIIIAQLBEHCQVPSARVPQPPAPAPRYVQPTVNRRIINQISTN 240
QY 241 EIGSQONLKVLPPLPTMTLTLSLSSDPSGPRDCLQLEDDHTSSIVYKPEENTN 300
DB 241 EIGSQONLKVLPPLPTMTLTLSLSSDPSGPRDCLQLEDDHTSSIVYKPEENTN 300
QY 301 RLMQVWCDQRDPCGWTYIQRRLDGSVNFRRMWTYKQGFNIDGYWLGJENIYWLTNQ 360
DB 301 RLMQVWCDQRDPCGWTYIQRRLDGSVNFRRMWTYKQGFNIDGYWLGJENIYWLTNQ 360
QY 361 GNYKLLVWMEWDSGRKVPFAEYASFLPESEYKRLRLRYHGNADSTFWNGKQFTLLD 420
DB 361 GNYKLLVWMEWDSGRKVPFAEYASFLPESEYKRLRLRYHGNADSTFWNGKQFTLLD 420
QY 421 RDHDVYTGCAHYQKGGWVYNACASNTNGVYRGHRSRQKQDVYAAEFRGGSYSLKK 480
DB 421 RDHDVYTGCAHYQKGGWVYNACASNTNGVYRGHRSRQKQDVYAAEFRGGSYSLKK 480
QY 481 VVMATIRPNENTFH 493
DB 481 VVMATIRPNENTFH 493

RESULT 15
ABU81003
ID ABU81003 standard, protein; 493 AA.

XX AC ABU81003;
XX DT 23-JUN-2003 (first entry)
XX DE Human PRO polypeptide #134.
XX KM Human; PRO polypeptide; secreted and transmembrane protein;
XX KM anti-PRO antibody; diagnostic assay; gene expression; diabetes;
XX KM bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
XX KM sports injury; osteoarthritis; hyper-insulinemia; hypo-insulinemia;
XX KM hearing loss; coagulation disorder; stroke; heart attack; cardiac;
XX KM antidiabetic; anorectic; vulnerability; antidiabetic; osteopathic;
XX KM antineumatic; auditory; cerebroprotective; angiogenic.
XX OS Homo sapiens.
XX PN US2003004311-A1.
XX PD 02-JAN-2003.
XX PF 19-DEC-2001; 2001US-00028072.
XX PR 18-JUN-1997; 97US-0049911P.
XX PR 26-AUG-1997; 97US-0056974P.
XX PR 17-SEP-1997; 97US-0059113P.
XX PR 17-SEP-1997; 97US-0059115P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 17-SEP-1997; 97US-0059122P.
XX PR 17-SEP-1997; 97US-0059184P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059352P.
XX PR 19-SEP-1997; 97US-0059588P.
XX PR 19-SEP-1997; 97US-0059836P.
XX PR 24-SEP-1997; 97US-0062280P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.
XX PR 17-OCT-1997; 97US-0063755P.
XX PR 24-OCT-1997; 97US-0062814P.
XX PR 24-OCT-1997; 97US-0063045P.
XX PR 24-OCT-1997; 97US-0063082P.
XX PR 24-OCT-1997; 97US-0063127P.
XX PR 27-OCT-1997; 97US-0063327P.
XX PR 27-OCT-1997; 97US-0063329P.
XX PR 28-OCT-1997; 97US-0063505P.
XX PR 28-OCT-1997; 97US-0063561P.
XX PR 29-OCT-1997; 97US-0063704P.
XX PR 29-OCT-1997; 97US-0063733P.
XX PR 29-OCT-1997; 97US-0063735P.
XX PR 29-OCT-1997; 97US-0063738P.
XX PR 03-NOV-1997; 97US-0064288P.
XX PR 07-NOV-1997; 97US-0064809P.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 17-NOV-1997; 97US-0065846P.
XX PR 21-NOV-1997; 97US-0066364P.
XX PR 24-NOV-1997; 97US-0066433P.
XX PR 24-NOV-1997; 97US-0066511P.
XX PR 24-NOV-1997; 97US-0066702P.
XX PR 11-DEC-1997; 97US-0069212P.
XX PR 11-DEC-1997; 97US-0069278P.
XX PR 11-DEC-1997; 97US-0069344P.
XX PR 16-DEC-1997; 97US-0069694P.
XX PR 23-JAN-1998; 98US-0072320P.
XX PR 04-FEB-1998; 98US-0073612P.
XX PR 09-FEB-1998; 98US-0074086P.
XX PR 09-FEB-1998; 98US-0074092P.
XX PR 12-MAR-1998; 98US-0077791P.
XX PR 20-MAR-1998; 98US-0078910P.
XX PR 25-MAR-1998; 98US-0079294P.
XX PR 27-MAR-1998; 98US-0079663P.
XX PR 31-MAR-1998; 98US-0079728P.
XX PR 31-MAR-1998; 98US-0080165P.

PR 12-JUN-1998; 98WO-US012456.
 PR 14-JUL-1998; 98WO-US014552.
 PR 28-AUG-1998; 98WO-US017888.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019093.
 PR 14-SEP-1998; 98WO-US019094.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 29-OCT-1998; 98WO-US022991.
 PR 29-OCT-1998; 98WO-US022992.
 PR 20-NOV-1998; 98WO-US024855.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 98WO-US000106.
 PR 08-MAR-1999; 98WO-US005028.
 PR 10-MAR-1999; 98WO-US005190.
 PR 20-APR-1999; 98WO-US008615.
 PR 14-MAY-1999; 98WO-US010733.
 PR 02-JUN-1999; 98WO-US012252.
 PR 01-SEP-1999; 98WO-US020111.
 PR 08-SEP-1999; 98WO-US020594.
 PR 13-SEP-1999; 98WO-US020944.
 PR 15-SEP-1999; 98WO-US021050.
 PR 15-SEP-1999; 98WO-US021547.
 PR 05-OCT-1999; 98WO-US023089.
 PR 29-NOV-1999; 98WO-US028214.
 PR 30-NOV-1999; 98WO-US028313.
 PR 30-NOV-1999; 98WO-US028409.
 PR 01-DEC-1999; 98WO-US028301.
 PR 01-DEC-1999; 98WO-US028634.
 PR 02-DEC-1999; 98WO-US028551.
 PR 02-DEC-1999; 98WO-US028564.
 PR 02-DEC-1999; 98WO-US028565.
 PR 16-DEC-1999; 98WO-US030095.
 PR 20-DEC-1999; 98WO-US030911.
 PR 20-DEC-1999; 98WO-US030999.
 PR 30-DEC-1999; 98WO-US031243.
 PR 30-DEC-1999; 98WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005746.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
 PI Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
 XX
 DR WPI; 2003-352836/33.
 DR N-PSDB; ACA67127.
 XX
 PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
 PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
 PT heart attack.
 XX
 PS Claim 12, Fig 268, 643pp; English.
 XX

CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO
 CC polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a medicament
 CC useful in the treatment of diabetes, bone and/or cartilage disorders
 CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
 CC hyper- or hypo-insulinemia, hearing loss, and coagulation disorders

CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells, tissues or
 CC serum, and for affinity purification of PRO from recombinant cell culture
 CC or natural sources. AB080870-AB081144 represent the human PRO
 CC polypeptides of the invention. Note: The sequence data for this patent
 CC was obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdidentry.html
 XX
 SQ Sequence 493 AA;

Query Match 99.9%; Score 2682; DB 6; Length 493;
 Best Local Similarity 99.8%; Pred. No. 1.4e-216;
 Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCMTLGLLAAAGVAGQDGEFGTEGSPREFYLYRRYRAGEGQCKYTFYV 60
 DB 1 MRPLCTCMTLGLLAAAGVAGQDGEFGTEGSPREFYLYRRYRAGEGQCKYTFYV 60
 QY 61 PQQRTGALCVNSKEPEVLENNRVHKOELNNELLKOKQIETLQQLVRYDGIYSEV 120
 DB 61 PQQRTGALCVNSKEPEVLENNRVHKOELNNELLKOKQIETLQQLVRYDGIYSEV 120
 QY 121 KLRKESRMNNSKVTLQYMLHEIRKRDNALELSOLENRLINQPADMLQASRYKOLE 180
 DB 121 KLRKESRMNNSKVTLQYMLHEIRKRDNALELSOLENRLINQPADMLQASRYKOLE 180
 QY 181 HKYQHLATLAHQSEIIAQLHEHCORVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
 DB 181 HKYQHLATLAHQSEIIAQLHEHCORVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
 QY 241 EIOSDONLKYLPPLPTMPTLTSLPSTDKSGPMDCQLALEDGHDSSITLVKPENTN 300
 DB 241 EIOSDONLKYLPPLPTMPTLTSLPSTDKSGPMDCQLALEDGHDSSITLVKPENTN 300
 QY 301 RLMQVWCDDRDHDPGGTIVQRRIDGSVNFPRMTEYKQSGNIDGMYLGENIYWLINQ 360
 DB 301 RLMQVWCDDRDHDPGGTIVQRRIDGSVNFPRMTEYKQSGNIDGMYLGENIYWLINQ 360
 QY 361 GNYKLLVTMEDWSGRVPAEYASFRLEPSEYKRLRGYHGNAGDSFTWHNGKQFTLD 420
 DB 361 GNYKLLVTMEDWSGRVPAEYASFRLEPSEYKRLRGYHGNAGDSFTWHNGKQFTLD 420
 QY 421 RQHDVYTGCAHYKQKGMVYNAQASHNLNGVYRGSHYRSRYQDGVYAAEPFGSGYSLKK 480
 DB 421 RQHDVYTGCAHYKQKGMVYNAQASHNLNGVYRGSHYRSRYQDGVYAAEPFGSGYSLKK 480
 QY 481 VVMIRPNPNTFH 493
 DB 481 VVMIRPNPNTFH 493

Search completed: July 30, 2004, 12:36:14
 Job time : 57 secs

QY 121 KLRKESRNNNSRVTLQYMLHEIIRKDNALIELSOLNRIINOTADMLQASXYKXLE 180
DB 121 KLRKESRNNNSRVTLQYMLHEIIRKDNALIELSOLNRIINOTADMLQASXYKXLE 180
QY 181 HKYQHLATLAHNOSEIIAOLEHCOQVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
DB 181 HKYQHLATLAHNOSEIIAOLEHCOQVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMWDCQALJEDGHTSSIVLVKRENTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMWDCQALJEDGHTSSIVLVKRENTN 300
QY 301 RLMQWCDORHDPGWTVIQRLDGSVNFPRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
DB 301 RLMQWCDORHDPGWTVIQRLDGSVNFPRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
QY 361 GNYKLVTMEDWSGKRVFAEYASFRLPESEYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
DB 361 GNYKLVTMEDWSGKRVFAEYASFRLPESEYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
QY 421 RHDVYTGNCAYQKQGMWYNACAHSNLNGVYRGHYSRYQDGYVMAEFPGGSYSLLK 480
DB 421 RHDVYTGNCAYQKQGMWYNACAHSNLNGVYRGHYSRYQDGYVMAEFPGGSYSLLK 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

RESULT 2

US-08-960-507-2
; Sequence 2, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,507
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-960-507-2

Query Match 99.9%; Score 2682; DB 3; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCVTCWMLGLLAAGAVAGQEDPEGETECSPREFFIYLNRYKAGSODKCTYTFIV 60
DB 1 MRPLCVTCWMLGLLAAGAVAGQEDPEGETECSPREFFIYLNRYKAGSODKCTYTFIV 60
QY 61 POORVTGATCVNSKEPEVLENNRVHKOELILNNELLKORJOETLQOLVKVQGGIVSEV 120
DB 61 POORVTGATCVNSKEPEVLENNRVHKOELILNNELLKORJOETLQOLVKVQGGIVSEV 120
QY 121 KLRKESRNNNSRVTLQYMLHEIIRKDNALIELSOLNRIINOTADMLQASXYKXLE 180
DB 121 KLRKESRNNNSRVTLQYMLHEIIRKDNALIELSOLNRIINOTADMLQASXYKXLE 180
QY 181 HKYQHLATLAHNOSEIIAOLEHCOQVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
DB 181 HKYQHLATLAHNOSEIIAOLEHCOQVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMWDCQALJEDGHTSSIVLVKRENTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMWDCQALJEDGHTSSIVLVKRENTN 300
QY 301 RLMQWCDORHDPGWTVIQRLDGSVNFPRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
DB 301 RLMQWCDORHDPGWTVIQRLDGSVNFPRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
QY 361 GNYKLVTMEDWSGKRVFAEYASFRLPESEYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
DB 361 GNYKLVTMEDWSGKRVFAEYASFRLPESEYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
QY 421 RHDVYTGNCAYQKQGMWYNACAHSNLNGVYRGHYSRYQDGYVMAEFPGGSYSLLK 480
DB 421 RHDVYTGNCAYQKQGMWYNACAHSNLNGVYRGHYSRYQDGYVMAEFPGGSYSLLK 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

RESULT 3

US-09-136-828-2
; Sequence 2, Application US/09136828
; Patent No. 6350450
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Tie Ligands
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,828
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1130RIA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 493 amino acids
; TYPE: Amino Acid

TOPOLOGY: Linear
US-09-136-828-2

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPLCTCWMGLLAANGAVAGGDEGEGTEGSPREFTYINRYKAGESODKCTYFTIV 60
DB 1 MRPLCTCWMGLLAANGAVAGGDEGEGTEGSPREFTYINRYKAGESODKCTYFTIV 60
QY 61 PQORVTGAI CVNSKEPEVLEENRVKQELINNNELKQKQIETLQOLVKGIVSEV 120
DB 61 PQORVTGAI CVNSKEPEVLEENRVKQELINNNELKQKQIETLQOLVKGIVSEV 120
QY 121 KILKRESNNNSRVTLQYMLHEITIRKDNALIELSOLENNRIINOTADMQLASKYKDL 180
DB 121 KILKRESNNNSRVTLQYMLHEITIRKDNALIELSOLENNRIINOTADMQLASKYKDL 180
QY 181 HKYQHLATLANHQSIIIAQLBEHCORVPSARVPQPPAPAPRYVQPTNRIINQISTN 240
DB 181 HKYQHLATLANHQSIIIAQLBEHCORVPSARVPQPPAPAPRYVQPTNRIINQISTN 240
QY 241 EIQSDQNLKVLPEPLPTMTLTSIPSSITDKPSGWRDCLQALBDGHTSSIIYVKEPNTN 300
DB 241 EIQSDQNLKVLPEPLPTMTLTSIPSSITDKPSGWRDCLQALBDGHTSSIIYVKEPNTN 300
QY 301 RLMQWCDORHDPGGWTVIQRLDGSVNFRRMNETYKQFGNIDGEYWLGENIYWLTNQ 360
DB 301 RLMQWCDORHDPGGWTVIQRLDGSVNFRRMNETYKQFGNIDGEYWLGENIYWLTNQ 360
QY 361 GNYKLVTMEDSGKRVFAEYASFLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLVTMEDSGKRVFAEYASFLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAYKQGGWYNACASHNLNGVYRGHYSRKYODGYVMAEFPGGSYSLKK 480
DB 421 RDHDVYTGNCAYKQGGWYNACASHNLNGVYRGHYSRKYODGYVMAEFPGGSYSLKK 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

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RESULT 4
US-09-332-928A-2
Sequence 2, Application US/09332928A
Patent No. 6368853

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

TITLE OF INVENTION: Tie Ligands

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 493 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-332-928A-2

Query Match 99.9%; Score 2682; DB 4; Length 493;

Best Local Similarity 99.8%; Pred. No. 4.8e-220;

Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPLCTCWMGLLAANGAVAGGDEGEGTEGSPREFTYINRYKAGESODKCTYFTIV 60
DB 1 MRPLCTCWMGLLAANGAVAGGDEGEGTEGSPREFTYINRYKAGESODKCTYFTIV 60
QY 61 PQORVTGAI CVNSKEPEVLEENRVKQELINNNELKQKQIETLQOLVKGIVSEV 120
DB 61 PQORVTGAI CVNSKEPEVLEENRVKQELINNNELKQKQIETLQOLVKGIVSEV 120
QY 121 KILKRESNNNSRVTLQYMLHEITIRKDNALIELSOLENNRIINOTADMQLASKYKDL 180
DB 121 KILKRESNNNSRVTLQYMLHEITIRKDNALIELSOLENNRIINOTADMQLASKYKDL 180
QY 181 HKYQHLATLANHQSIIIAQLBEHCORVPSARVPQPPAPAPRYVQPTNRIINQISTN 240
DB 181 HKYQHLATLANHQSIIIAQLBEHCORVPSARVPQPPAPAPRYVQPTNRIINQISTN 240
QY 241 EIQSDQNLKVLPEPLPTMTLTSIPSSITDKPSGWRDCLQALBDGHTSSIIYVKEPNTN 300
DB 241 EIQSDQNLKVLPEPLPTMTLTSIPSSITDKPSGWRDCLQALBDGHTSSIIYVKEPNTN 300
QY 301 RLMQWCDORHDPGGWTVIQRLDGSVNFRRMNETYKQFGNIDGEYWLGENIYWLTNQ 360
DB 301 RLMQWCDORHDPGGWTVIQRLDGSVNFRRMNETYKQFGNIDGEYWLGENIYWLTNQ 360
QY 361 GNYKLVTMEDSGKRVFAEYASFLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLVTMEDSGKRVFAEYASFLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAYKQGGWYNACASHNLNGVYRGHYSRKYODGYVMAEFPGGSYSLKK 480
DB 421 RDHDVYTGNCAYKQGGWYNACASHNLNGVYRGHYSRKYODGYVMAEFPGGSYSLKK 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

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RESULT 5
US-09-136-801-2
Sequence 2, Application US/09136801
Patent No. 6413770

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth

APPLICANT: Botstein, David

APPLICANT: Goddard, Audrey

APPLICANT: Roy, Margaret

APPLICANT: Ferrara, Napoleone

APPLICANT: Tuma, Daniel

APPLICANT: Schwall, Ralph

TITLE OF INVENTION: Tie Ligand Homologues

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPac (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,801
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P130P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-136-801-2

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLLAAAGVAGQEDGFEETEGSPREFIYLRKVRAGSSQCKCTYFTIV 60
DB 1 MRPLCTCWMGLLAAAGVAGQEDGFEETEGSPREFIYLRKVRAGSSQCKCTYFTIV 60
QY 61 PQORVTGALCVNSKEPEVLLENRVHKOELNNELLKOKROIELTQOLVAVDGIIVSEV 120
DB 61 PQORVTGALCVNSKEPEVLLENRVHKOELNNELLKOKROIELTQOLVAVDGIIVSEV 120
QY 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRIINOTADWLQASRYKQLE 180
DB 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRIINOTADWLQASRYKQLE 180
QY 181 HKYOHATLAHNSSEIIAQLHEHCQVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
DB 181 HKYOHATLAHNSSEIIAQLHEHCQVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMDCLOALEDHDTSSIYLKPEENTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMDCLOALEDHDTSSIYLKPEENTN 300
QY 301 RLMOVWCDORHDPGQMTVIQRRLDGSVNFRRWETTYKQFGNIDGYWLGLENITWLTNQ 360
DB 301 RLMOVWCDORHDPGQMTVIQRRLDGSVNFRRWETTYKQFGNIDGYWLGLENITWLTNQ 360
QY 361 GNYKLVITMEDWSGKRVFAEYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLVITMEDWSGKRVFAEYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RHDVYTGCAHYQKGGWYNA CAHSNLTNGVYRGGHYRSRYODGVYAAEFRGGSYSILKK 480
DB 421 RHDVYTGCAHYQKGGWYNA CAHSNLTNGVYRGGHYRSRYODGVYAAEFRGGSYSILKK 480
QY 481 VYMMIRPNNTFH 493
DB 481 VYMMIRPNNTFH 493

RESULT 6
US-09-332-929-2
Sequence 2, Application US/09332929
Patent No. 6420542

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: The ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPac (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-332-929-2

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLLAAAGVAGQEDGFEETEGSPREFIYLRKVRAGSSQCKCTYFTIV 60
DB 1 MRPLCTCWMGLLAAAGVAGQEDGFEETEGSPREFIYLRKVRAGSSQCKCTYFTIV 60
QY 61 PQORVTGALCVNSKEPEVLLENRVHKOELNNELLKOKROIELTQOLVAVDGIIVSEV 120
DB 61 PQORVTGALCVNSKEPEVLLENRVHKOELNNELLKOKROIELTQOLVAVDGIIVSEV 120
QY 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRIINOTADWLQASRYKQLE 180
DB 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRIINOTADWLQASRYKQLE 180
QY 181 HKYOHATLAHNSSEIIAQLHEHCQVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
DB 181 HKYOHATLAHNSSEIIAQLHEHCQVPSARVPQPPAPPRVYQPTYNRIINQISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMDCLOALEDHDTSSIYLKPEENTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSTDKPSGPMDCLOALEDHDTSSIYLKPEENTN 300
QY 301 RLMOVWCDORHDPGQMTVIQRRLDGSVNFRRWETTYKQFGNIDGYWLGLENITWLTNQ 360
DB 301 RLMOVWCDORHDPGQMTVIQRRLDGSVNFRRWETTYKQFGNIDGYWLGLENITWLTNQ 360
QY 361 GNYKLVITMEDWSGKRVFAEYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLVITMEDWSGKRVFAEYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RHDVYTGCAHYQKGGWYNA CAHSNLTNGVYRGGHYRSRYODGVYAAEFRGGSYSILKK 480
DB 421 RHDVYTGCAHYQKGGWYNA CAHSNLTNGVYRGGHYRSRYODGVYAAEFRGGSYSILKK 480

QY 481 VMMIRPENTFH 493
DB 481 VMMIRPENTFH 493

RESULT 7
US-09-333-075-2
Sequence 2, Application US/09333075
Patent No. 6482331
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,075
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-333-075-2

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWLGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
DB 1 MRPLCTCWLGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
QY 61 POORVTGALCVNSKEEVLLENRVHKOELINNELLKOKROIETLQOLVEVDGIVSEV 120
DB 61 POORVTGALCVNSKEEVLLENRVHKOELINNELLKOKROIETLQOLVEVDGIVSEV 120
QY 121 KLIRKESRNNSRVTOLYMOLEHEIRKRDNALELSOLENRIINQADMLQASXYKDL 180
DB 121 KLIRKESRNNSRVTOLYMOLEHEIRKRDNALELSOLENRIINQADMLQASXYKDL 180
QY 181 HKYOHATLANOSEIILAOLEEHQORVPSPAPVOPPPAPPRVYQPTNYRIINOISTN 240
DB 181 HKYOHATLANOSEIILAOLEEHQORVPSPAPVOPPPAPPRVYQPTNYRIINOISTN 240
QY 241 EIISDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCQALBDGHTSSIYLVKPENTN 300
DB 241 EIISDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCQALBDGHTSSIYLVKPENTN 300
QY 301 RLMQVWCDQRHDPGQWTVIQRLDGSVNFPRNMETTYKQFGNIDGEYWLGLENIYWLTLNQ 360

DB 301 RLMQVWCDQRHDPGQWTVIQRLDGSVNFPRNMETTYKQFGNIDGEYWLGLENIYWLTLNQ 360
QY 361 GNYKLVTMEDWSGRKYPAEYASFRLEPSEYKRLRGYHGNAGDSFTWNGKQFTLTD 420
DB 361 GNYKLVTMEDWSGRKYPAEYASFRLEPSEYKRLRGYHGNAGDSFTWNGKQFTLTD 420
QY 421 RDHDVYTGNCANHYKQSGMWTYNACASHNLANGWYRGHRSRYODGVYMAEFRRGGSYSLKK 480
DB 421 RDHDVYTGNCANHYKQSGMWTYNACASHNLANGWYRGHRSRYODGVYMAEFRRGGSYSLKK 480
QY 481 VMMIRPENTFH 493
DB 481 VMMIRPENTFH 493

RESULT 8
US-09-202-088A-2
Sequence 2, Application US/09202088A
Patent No. 6551822
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Boctstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
FILE REFERENCE: P1130P3US
CURRENT APPLICATION NUMBER: US/09/202,088A
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 2
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-202-088A-2

Query Match 99.9%; Score 2682; DB 4; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.8e-220;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWLGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
DB 1 MRPLCTCWLGLLAAGAVAGQEDGEGTEGSPREFIYLNRYKAGESQDKCTYTFIV 60
QY 61 POORVTGALCVNSKEEVLLENRVHKOELINNELLKOKROIETLQOLVEVDGIVSEV 120
DB 61 POORVTGALCVNSKEEVLLENRVHKOELINNELLKOKROIETLQOLVEVDGIVSEV 120
QY 121 KLIRKESRNNSRVTOLYMOLEHEIRKRDNALELSOLENRIINQADMLQASXYKDL 180
DB 121 KLIRKESRNNSRVTOLYMOLEHEIRKRDNALELSOLENRIINQADMLQASXYKDL 180
QY 181 HKYOHATLANOSEIILAOLEEHQORVPSPAPVOPPPAPPRVYQPTNYRIINOISTN 240
DB 181 HKYOHATLANOSEIILAOLEEHQORVPSPAPVOPPPAPPRVYQPTNYRIINOISTN 240
QY 241 EIISDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCQALBDGHTSSIYLVKPENTN 300
DB 241 EIISDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCQALBDGHTSSIYLVKPENTN 300
QY 301 RLMQVWCDQRHDPGQWTVIQRLDGSVNFPRNMETTYKQFGNIDGEYWLGLENIYWLTLNQ 360
DB 301 RLMQVWCDQRHDPGQWTVIQRLDGSVNFPRNMETTYKQFGNIDGEYWLGLENIYWLTLNQ 360
QY 361 GNYKLVTMEDWSGRKYPAEYASFRLEPSEYKRLRGYHGNAGDSFTWNGKQFTLTD 420

Db 361 GNYKLVTWEDWSGRKVFAYASFRLEPSEYKLTGRYHGNAGDSFTWHNGKQFTTLD 420
 Qy 421 RDHDVYTGNCAHYOKGGMWYNACAHSNLNGWYRGHYSRYPDGYVMAEFRRGSYSLLK 480
 Db 421 RDHDVYTGNCAHYOKGGMWYNACAHSNLNGWYRGHYSRYPDGYVMAEFRRGSYSLLK 480
 Qy 481 VMMIRPNPNTFH 493
 Db 481 VMMIRPNPNTFH 493

RESULT 9

US-09-333-077-2
 ; Sequence 2, Application US/09333077
 ; Patent No. 6586397
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; TITLE OF INVENTION: Tie Ligands
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPacIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/333,077
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/933,821
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P1130
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-3216
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 493 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: linear
 ; US-09-333-077-2

Query Match 99.9%; Score 2662; DB 4; Length 493;
 Best Local Similarity 99.8%; Pred. No. 4.8e-220;
 Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MBLPCTCWMGLLAAAGVAGQEDGFEETGSGPREFTYINRYRABESODKCTYFTIV 60
 Db 1 MBLPCTCWMGLLAAAGVAGQEDGFEETGSGPREFTYINRYRABESODKCTYFTIV 60
 Qy 61 PQRVTGALCVNSKEPEVLLNRVAKOELINLNNLKKQKQIETLQQLVAVDGGIVSEV 120
 Db 61 PQRVTGALCVNSKEPEVLLNRVAKOELINLNNLKKQKQIETLQQLVAVDGGIVSEV 120
 Qy 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRLINQTAQMLQSLASKYKDL 180
 Db 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRLINQTAQMLQSLASKYKDL 180
 Qy 181 HKYQHLATLAAHQSEILIAQLEEHQCVPSARVPQPPAPPRVYQPTVRIINQISTN 240
 Db 181 HKYQHLATLAAHQSEILIAQLEEHQCVPSARVPQPPAPPRVYQPTVRIINQISTN 240

Qy 241 EIOGDQNLKYLPPPLPTMPTLTSLPSTDKPSGPMWDCQALBEDGHTSSIVLKEPENTN 300
 Db 241 EIOGDQNLKYLPPPLPTMPTLTSLPSTDKPSGPMWDCQALBEDGHTSSIVLKEPENTN 300
 Qy 301 RLMOVWCDQHRHDPGCVTVIQRIDGVSVPFRMETTKQGFNGIDGYWMLGLENTYVLNQ 360
 Db 301 RLMOVWCDQHRHDPGCVTVIQRIDGVSVPFRMETTKQGFNGIDGYWMLGLENTYVLNQ 360
 Qy 361 GNYKLVTWEDWSGRKVFAYASFRLEPSEYKLTGRYHGNAGDSFTWHNGKQFTTLD 420
 Db 361 GNYKLVTWEDWSGRKVFAYASFRLEPSEYKLTGRYHGNAGDSFTWHNGKQFTTLD 420
 Qy 421 RDHDVYTGNCAHYOKGGMWYNACAHSNLNGWYRGHYSRYPDGYVMAEFRRGSYSLLK 480
 Db 421 RDHDVYTGNCAHYOKGGMWYNACAHSNLNGWYRGHYSRYPDGYVMAEFRRGSYSLLK 480
 Qy 481 VMMIRPNPNTFH 493
 Db 481 VMMIRPNPNTFH 493

RESULT 10

US-08-933-821-4
 ; Sequence 4, Application US/08933821
 ; Patent No. 5972338
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; TITLE OF INVENTION: Tie Ligands
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPacIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/933,821
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Ginger R.
 ; REGISTRATION NUMBER: 33,055
 ; REFERENCE/DOCKET NUMBER: P1130
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-3216
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 491 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: linear
 ; US-08-933-821-4

Query Match 56.1%; Score 1507.5; DB 2; Length 491;
 Best Local Similarity 58.6%; Pred. No. 5e-120;
 Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;
 Qy 9 WILGLLAAAGVAGQSDGFEETGSGPREFTYINRYRABESOD--KCTYFTIVP 61
 Db 6 WILGLVFLPLVDTGHRG-----GQFKIKKINQRYPPATIDKEAKKCAVTFIVP 56
 Qy 62 QQRVTGALCVNSKEPEV-ILNRVAKOELINLNNLKKQKQIETLQQLVAVDGGIVSEV 120
 Db 57 QQRITPTICVTGQQAASITIKDITMDLENLKDVLRSQREIDVLQLVVDGAINVNEV 116
 Qy 121 KILRKESRMNSRVTLQVQLLHEIIRKDNALLESQLENRLINQTAQMLQSLASKYKDL 180

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Query Match          56.1%; Score 1507.5; DB 3; Length 491;
Best Local Similarity 58.6%; Pred. No. 56-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9

QY 9 WMLGLLMMAGNVAQGDDEGEGEGEESPPRF-----IYLNRKYKAGESQD---KCTYTFIYP 61
  | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

1 APPLICANT: Godowski, Paul J.
 2 APPLICANT: Gurney, Austin L.
 3 TITLE OF INVENTION: Tie Ligands
 4 NUMBER OF SEQUENCES: 17
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Genentech, Inc.
 7 STREET: 1 DNA Way
 8 CITY: South San Francisco
 9 STATE: California
 10 COUNTRY: USA
 11 ZIP: 94080
 12
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC-DOS/MS-DOS
 17 SOFTWARE: WinPatIn (Genentech)
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/09/136,828
 20 FILING DATE:
 21 CLASSIFICATION:
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: Dreger, Ginger R.
 24 REGISTRATION NUMBER: 33,055
 25 REFERENCE/DOCKET NUMBER: P11301A
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: 650/225-3216
 28 TELEFAX: 650/952-9881
 29 INFORMATION FOR SEQ ID NO: 4:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 491 amino acids
 32 TYPE: amino acid
 33 TOPOLOGY: linear
 34
 35 US-09-136-828-4

Query Match 56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

9 WMLGLAAGAVAGGDEGFEETEGSPREF---IYNRYKAGESOD---KCTYFTVP 61
6 WMLGLVFLVLDVTHGCRG-----GQFKIKINQRRYPRATGKEAKKCAVTFVLP 56
62 QQRVTGALCVNSKEPEV-ILENRVHKQELINNELKQKQIETLQOLVKYDGIIVSEV 120
57 EGRITGICVNTKGQDASTIKDMITMDLENLKDVLRSQREIDVLQVVDGNTVNEV 116
121 KLRKESRMNSRVTLQVQLHEIRKDNALLESOLENRLINOTADMLOLASKYKYLE 180
117 KLRKESRMNSRVTLQVQLHEIRKDNALLESOLENKLINTTETMLKATRYRELE 176
181 HKYQHLATLANQSEITIAOLEEHQORVPSARVPQPP---AAPRVYQPTYNRIINQI 237
177 VKYASLTDLVNNSQVMTLLEEQCLIRFSRQDTHVSPPLVQVVPQHI--PNSQYTPGLL 234
238 STNEIOSDQNL--KVLPP-LPTMPLT--SLPSSTDKSGPWRDCLQLEDGHTSSLY 292
235 GGEIORDPGYPRDLMPPLDLATSPKSPFKIPVTFINEGPFKDCQAKKAGHSVSGIY 294
293 LVKPENTNRLMOVWCQORHDPGWTVIQRLDGSVNFPMNMYKQGFNIDGSEYVLGLE 352
295 MKPENSNGPMQJMCENS.LDPGWTVIQKRTDGSVNFPMNMYKQGFNIDGSEYVLGLE 354
353 NIYMLTNGQNYKLLVTMEDNSGRKVPAAEYASFLRPESEFYKLRGRHGNAGDSFTWEN 412
355 NIYMLTNGQNYKLLVLEBMSDKKYAEYSSFLRPESEFYRLRTGYQGNAGDSMMWEN 414
413 GKQFTLDRDHDVYTGNCAYQKGMWYNACAHSNLNGVWYRGHYSRQYDGVYAAER 472
415 GKQFTLDRDHDVYTGNCAYQKGMWYNACAHSNLNGVWYRGHYSRQYDGVYAAER 474
473 GGSYSLKVVMMIRP 487
475 GGSYSLRAYQMMIKP 489

RESULT 13
US-09-332-928A-4
Sequence 4, Application US/09332928A
Patent No. 6368853
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,928A
FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Diegel, Ginger R.
REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-332-928A-4

Query Match 56.1%; Score 1507.5; DB 4; Length 491;
Best Local Similarity 58.6%; Pred. No. 5e-120;
Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

9 WMLGLAAGAVAGGDEGFEETEGSPREF---IYNRYKAGESOD---KCTYFTVP 61
6 WMLGLVFLVLDVTHGCRG-----GQFKIKINQRRYPRATGKEAKKCAVTFVLP 56
62 QQRVTGALCVNSKEPEV-ILENRVHKQELINNELKQKQIETLQOLVKYDGIIVSEV 120
57 EGRITGICVNTKGQDASTIKDMITMDLENLKDVLRSQREIDVLQVVDGNTVNEV 116
121 KLRKESRMNSRVTLQVQLHEIRKDNALLESOLENRLINOTADMLOLASKYKYLE 180
117 KLRKESRMNSRVTLQVQLHEIRKDNALLESOLENKLINTTETMLKATRYRELE 176
181 HKYQHLATLANQSEITIAOLEEHQORVPSARVPQPP---AAPRVYQPTYNRIINQI 237
177 VKYASLTDLVNNSQVMTLLEEQCLIRFSRQDTHVSPPLVQVVPQHI--PNSQYTPGLL 234
238 STNEIOSDQNL--KVLPP-LPTMPLT--SLPSSTDKSGPWRDCLQLEDGHTSSLY 292
235 GGEIORDPGYPRDLMPPLDLATSPKSPFKIPVTFINEGPFKDCQAKKAGHSVSGIY 294
293 LVKPENTNRLMOVWCQORHDPGWTVIQRLDGSVNFPMNMYKQGFNIDGSEYVLGLE 352
295 MKPENSNGPMQJMCENS.LDPGWTVIQKRTDGSVNFPMNMYKQGFNIDGSEYVLGLE 354
353 NIYMLTNGQNYKLLVTMEDNSGRKVPAAEYASFLRPESEFYKLRGRHGNAGDSFTWEN 412
355 NIYMLTNGQNYKLLVLEBMSDKKYAEYSSFLRPESEFYRLRTGYQGNAGDSMMWEN 414
413 GKQFTLDRDHDVYTGNCAYQKGMWYNACAHSNLNGVWYRGHYSRQYDGVYAAER 472
415 GKQFTLDRDHDVYTGNCAYQKGMWYNACAHSNLNGVWYRGHYSRQYDGVYAAER 474
473 GGSYSLKVVMMIRP 487
475 GGSYSLRAYQMMIKP 489

RESULT 14
US-09-136-801-4
Sequence 4, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
Gurney, Austin L.
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,801
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 491 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-136-801-4

Query Match 56.1%; Score 1507.5; DB 4; Length 491;
 Best Local Similarity 58.6%; Pred. No. 58-120;
 Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

9 WMLGLAAMGAVAGQEDGEGTEGSPREF---IYNRYKAGESQD---KCTYFTIVP 61
 6 WTLGVLFLLVDTGHCGRG-----GQFKIKINRRPRATDGEKKAAYTLFVP 56
 62 QQRVTGATCVNSKEPEV-LEENRVHKOELLNELIKOKROETTLQOLYKVDGIVSEV 120
 57 EGRITGICVNTKQDASTIKMTTRMDLENLKDVLRSQRKEIDVLQLVVDVGNIVNEV 116
 121 KLRKESRNNMSRVTLQYMLLHEIRKRDNALELSOLENRIINQADMLQLASKYKDL 180
 117 KLRKESRNNMSRVTLQYMLLHEIRKRDNSLELSOLENKILNVTTEMLKATRYELE 176
 181 HKYQHLATLANOSEILIAOLEHRCORVPSARVPQPP---AAPRYOPTYNRIINQI 237
 177 VKYASITDLVNNQSVMTLLEEQCLRIFSRODTHVSPPLVQVVPQHI--PNSQCYTPGL 234
 238 STNEIGSDQNL--KVLPPP-LPTMPTLT--SLPSTDKSGPWRDCLQALDGDHTSSIT 292
 235 GGNELIQDQVPRDLMPPLDLSPTKSPFKIPVTFINEGPFKCCQAKKEGHSVSGIT 294
 293 LVKPEENTRLMQVWCORHDPGWTVIQRLDGSVNFERNMETYKQGFNIDGEYWLGLE 352
 295 MKPEPNSNGPQMLCENSLDPGWTVIQKRTDGSVNFERNMENYKGFNIDGEYWLGLE 354
 353 NIYWLTLNQGNTKLLVTMEDWSGRKVPFAEYASFRLEPSESEYKRLRGYHNGAGSFTWHN 412
 355 NIYWLTLNQGNTKLLVTMEDWSGRKVPFAEYASFRLEPSESEYKRLRGYHNGAGSFTWHN 414
 413 GKQFTTLDHDDVYVTGNCAYOKQGWVYNAACASHNLNGVYRGHYRSRYODGVYMAEFR 472
 415 GKQFTTLDHDDVYVTGNCAYOKQGWVYNAACASHNLNGVYRGHYRSRYODGVYMAEFR 474
 473 GGSYSLLKVVVMIRP 487
 475 GGSYSLLRAVQMMIKP 489

RESULT 15
 US-09-332-929-4
 Sequence 4, Application US/09332929
 Patent No. 6420542
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: The Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/332,929
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/933,821
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/952-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 491 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-09-332-929-4

Query Match 56.1%; Score 1507.5; DB 4; Length 491;
 Best Local Similarity 58.6%; Pred. No. 58-120;
 Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

9 WMLGLAAMGAVAGQEDGEGTEGSPREF---IYNRYKAGESQD---KCTYFTIVP 61
 6 WTLGVLFLLVDTGHCGRG-----GQFKIKINRRPRATDGEKKAAYTLFVP 56
 62 QQRVTGATCVNSKEPEV-LEENRVHKOELLNELIKOKROETTLQOLYKVDGIVSEV 120
 57 EGRITGICVNTKQDASTIKMTTRMDLENLKDVLRSQRKEIDVLQLVVDVGNIVNEV 116
 121 KLRKESRNNMSRVTLQYMLLHEIRKRDNALELSOLENRIINQADMLQLASKYKDL 180
 117 KLRKESRNNMSRVTLQYMLLHEIRKRDNSLELSOLENKILNVTTEMLKATRYELE 176
 181 HKYQHLATLANOSEILIAOLEHRCORVPSARVPQPP---AAPRYOPTYNRIINQI 237
 177 VKYASITDLVNNQSVMTLLEEQCLRIFSRODTHVSPPLVQVVPQHI--PNSQCYTPGL 234
 238 STNEIGSDQNL--KVLPPP-LPTMPTLT--SLPSTDKSGPWRDCLQALDGDHTSSIT 292
 235 GGNELIQDQVPRDLMPPLDLSPTKSPFKIPVTFINEGPFKCCQAKKEGHSVSGIT 294
 293 LVKPEENTRLMQVWCORHDPGWTVIQRLDGSVNFERNMETYKQGFNIDGEYWLGLE 352
 295 MKPEPNSNGPQMLCENSLDPGWTVIQKRTDGSVNFERNMENYKGFNIDGEYWLGLE 354
 353 NIYWLTLNQGNTKLLVTMEDWSGRKVPFAEYASFRLEPSESEYKRLRGYHNGAGSFTWHN 412
 355 NIYWLTLNQGNTKLLVTMEDWSGRKVPFAEYASFRLEPSESEYKRLRGYHNGAGSFTWHN 414
 413 GKQFTTLDHDDVYVTGNCAYOKQGWVYNAACASHNLNGVYRGHYRSRYODGVYMAEFR 472
 415 GKQFTTLDHDDVYVTGNCAYOKQGWVYNAACASHNLNGVYRGHYRSRYODGVYMAEFR 474
 473 GGSYSLLKVVVMIRP 487

Db 475 GGSYSLRAYQMMKP 489

Search completed: July 30, 2004, 12:38:31
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2004, 12:37:34 ; Search time 46 Seconds
(without alignments)
3361.863 Million cell updates/sec

Title: US-10-018-386-2

Sequence: 1 MRPLCVTCMWGLLAAMGAV.....GSYSLKXVMWIRNPNTFH 493

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpa/PC1_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpa/US06_NEW_PUB.pep:*
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- 7: /cgn2_6/ptodata/1/pubpa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpa/US08_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2682	99.9	493	9	US-09-818-143-23
2	2682	99.9	493	10	US-09-832-355A-113
3	2682	99.9	493	10	US-09-983-000A-8
4	2682	99.9	493	12	US-10-147-493-268
5	2682	99.9	493	12	US-10-145-127-268
6	2682	99.9	493	12	US-10-160-503-268
7	2682	99.9	493	12	US-10-143-118-268
8	2682	99.9	493	12	US-10-144-993-268
9	2682	99.9	493	12	US-10-158-787-268
10	2682	99.9	493	12	US-10-140-024-268
11	2682	99.9	493	12	US-10-140-808-268
12	2682	99.9	493	12	US-10-157-405-268
13	2682	99.9	493	12	US-10-127-852A-268
14	2682	99.9	493	12	US-10-127-900A-268
15	2682	99.9	493	12	US-10-128-685A-268

16	2682	99.9	493	12	US-10-131-820A-268	Sequence 268, App
17	2682	99.9	493	12	US-10-142-886-268	Sequence 268, App
18	2682	99.9	493	12	US-10-146-728-268	Sequence 268, App
19	2682	99.9	493	12	US-10-146-786-268	Sequence 268, App
20	2682	99.9	493	12	US-10-147-499-268	Sequence 268, App
21	2682	99.9	493	12	US-10-157-798-268	Sequence 268, App
22	2682	99.9	493	13	US-10-066-500-4	Sequence 4, Appl
23	2682	99.9	493	14	US-10-028-072-268	Sequence 268, App
24	2682	99.9	493	14	US-10-121-045-268	Sequence 268, App
25	2682	99.9	493	14	US-10-123-904-268	Sequence 268, App
26	2682	99.9	493	14	US-10-140-470-268	Sequence 268, App
27	2682	99.9	493	14	US-10-175-746-268	Sequence 268, App
28	2682	99.9	493	14	US-10-176-918-268	Sequence 268, App
29	2682	99.9	493	14	US-10-176-921-268	Sequence 268, App
30	2682	99.9	493	14	US-10-002-796-4	Sequence 4, Appl
31	2682	99.9	493	14	US-10-066-273-4	Sequence 4, Appl
32	2682	99.9	493	14	US-10-066-494-4	Sequence 4, Appl
33	2682	99.9	493	14	US-10-137-865-268	Sequence 268, App
34	2682	99.9	493	14	US-10-140-474-268	Sequence 268, App
35	2682	99.9	493	14	US-10-142-431-268	Sequence 268, App
36	2682	99.9	493	14	US-10-143-114-268	Sequence 268, App
37	2682	99.9	493	14	US-10-140-002-268	Sequence 268, App
38	2682	99.9	493	14	US-10-066-269-4	Sequence 4, Appl
39	2682	99.9	493	14	US-10-066-211-4	Sequence 4, Appl
40	2682	99.9	493	14	US-10-066-193-4	Sequence 4, Appl
41	2682	99.9	493	14	US-10-142-419-268	Sequence 268, App
42	2682	99.9	493	14	US-10-123-262-268	Sequence 268, App
43	2682	99.9	493	14	US-10-142-423-268	Sequence 268, App
44	2682	99.9	493	14	US-10-121-050-268	Sequence 268, App
45	2682	99.9	493	14	US-10-141-735-268	Sequence 268, App

ALIGNMENTS

RESULT 1
US-09-818-143-23
; Sequence 23, Application US/09818143
; Patent No. US2002019000A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
; FILE REFERENCE: PB-0004 CIP
; CURRENT APPLICATION NUMBER: US/09/818,143
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 23
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2268890C0D1
US-09-818-143-23

Query Match 99.9%; Score 2682; DB 9; Length 493;
Best local similarity 99.8%; Pred. No. 4.9e-210;
Matches 493; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRPLCVTCMWGLLAAMGAVAGGDDGGEGEGSPREFITLNYKKAAGSODKCTYTFIV	60
DB	1	MRPLCVTCMWGLLAAMGAVAGGDDGGEGEGSPREFITLNYKKAAGSODKCTYTFIV	60
QY	61	POQVITGALVNSKEPEVLLIENRHHKQELINNNELIKQKQIETIQOVLKVDGIVSEV	120
DB	61	POQVITGALVNSKEPEVLLIENRHHKQELINNNELIKQKQIETIQOVLKVDGIVSEV	120
QY	121	KLKRSERNNSRVTOIYVOLLHEITRKRDNALELSOLERIINOTADMQLASKYKDL	180
DB	121	KLKRSERNNSRVTOIYVOLLHEITRKRDNALELSOLERIINOTADMQLASKYKDL	180

QY 181 HKYCHLATHANOSSEIIAQLSEHCORVPSARVPQPPAAPRYQPPTYNRITINOISTN 240
DB 181 HKYCHLATHANOSSEIIAQLSEHCORVPSARVPQPPAAPRYQPPTYNRITINOISTN 240
QY 241 EIQSDONLKVLPPLPTMTLTSLPSSTDKPSGPRDCLQALDEGHTSSILYVKEPENTN 300
DB 241 EIQSDONLKVLPPLPTMTLTSLPSSTDKPSGPRDCLQALDEGHTSSILYVKEPENTN 300
QY 301 RLMQVWCORHDPGPGWTVYQRLDGSVNFPRWETRYKQGFNGTIDSEYWLGLENTYWLTNQ 360
DB 301 RLMQVWCORHDPGPGWTVYQRLDGSVNFPRWETRYKQGFNGTIDSEYWLGLENTYWLTNQ 360
QY 361 GNYKLLVTMEDWSGKRVFAEYASFRLEPESEYYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLLVTMEDWSGKRVFAEYASFRLEPESEYYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGCAHYQKQGWYTNACAHSNLNGWYRGCHYRSRYQDGYVAEFPGGSYSLSKK 480
DB 421 RDHDVYTGCAHYQKQGWYTNACAHSNLNGWYRGCHYRSRYQDGYVAEFPGGSYSLSKK 480
QY 481 VMMWIRPNPTFFH 493
DB 481 VMMWIRPNPTFFH 493

RESULT 2

US-09-832-355A-113
; Sequence 113, Application US/09832355A
; Publication No. US2003002751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-355A-113

Query Match 99.9%; Score 2682; DB 10; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCVTCWMLGLILAMGAVAGQDGFEGTEGSPREFIYLNRYKRGESQDKCTYTFIV 60
DB 1 MRPLCVTCWMLGLILAMGAVAGQDGFEGTEGSPREFIYLNRYKRGESQDKCTYTFIV 60
QY 61 POORVTGALCVNSKEPEVLENNRVHAKQELINNELLNQKQIETLQOLVYVDGIVSEV 120
DB 61 POORVTGALCVNSKEPEVLENNRVHAKQELINNELLNQKQIETLQOLVYVDGIVSEV 120
QY 121 KILRKESRMNSRVQOLVYQOLLEHIIKRDNLLEISQLENRIINQADMLQASXYKDE 180
DB 121 KILRKESRMNSRVQOLVYQOLLEHIIKRDNLLEISQLENRIINQADMLQASXYKDE 180
QY 181 HKYCHLATHANOSSEIIAQLSEHCORVPSARVPQPPAAPRYQPPTYNRITINOISTN 240
DB 181 HKYCHLATHANOSSEIIAQLSEHCORVPSARVPQPPAAPRYQPPTYNRITINOISTN 240
QY 241 EIQSDONLKVLPPLPTMTLTSLPSSTDKPSGPRDCLQALDEGHTSSILYVKEPENTN 300
DB 241 EIQSDONLKVLPPLPTMTLTSLPSSTDKPSGPRDCLQALDEGHTSSILYVKEPENTN 300
QY 301 RLMQVWCORHDPGPGWTVYQRLDGSVNFPRWETRYKQGFNGTIDSEYWLGLENTYWLTNQ 360
DB 301 RLMQVWCORHDPGPGWTVYQRLDGSVNFPRWETRYKQGFNGTIDSEYWLGLENTYWLTNQ 360
QY 361 GNYKLLVTMEDWSGKRVFAEYASFRLEPESEYYKRLGRYHGNAGDSFTWNGKQFTTLD 420

DB 361 GNYKLLVTMEDWSGKRVFAEYASFRLEPESEYYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGCAHYQKQGWYTNACAHSNLNGWYRGCHYRSRYQDGYVAEFPGGSYSLSKK 480
DB 421 RDHDVYTGCAHYQKQGWYTNACAHSNLNGWYRGCHYRSRYQDGYVAEFPGGSYSLSKK 480
QY 481 VMMWIRPNPTFFH 493
DB 481 VMMWIRPNPTFFH 493

RESULT 3

US-09-983-000A-8
; Sequence 8, Application US/0983000A
; Publication No. US20030118585A1
; GENERAL INFORMATION:
; APPLICANT: Agi Therapeutics
; APPLICANT: Melcher, Thorsten
; APPLICANT: Mueller, Sabine
; APPLICANT: Chin, Daniel
; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZA
; TITLE OF INVENTION: OF BRAIN TUMORS
; FILE REFERENCE: 263/180 -- Peaglamen -- AGY
; CURRENT APPLICATION NUMBER: US/09/983,000A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: gene (493)
; LOCATION: (1)..(493)
; OTHER INFORMATION: Angiopoietin-like 2 (ANGPTL2), protein
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: Potential
; NAME/KEY: CHAIN
; LOCATION: (23)..(493)
; OTHER INFORMATION: Angiopoietin-related protein 2
; NAME/KEY: DOMAIN
; LOCATION: (76)..(115)
; OTHER INFORMATION: Coiled Coil (potential)
; NAME/KEY: DOMAIN
; LOCATION: (152)..(206)
; OTHER INFORMATION: Coiled Coil (potential)
; NAME/KEY: DOMAIN
; LOCATION: (438)..(450)
; OTHER INFORMATION: Fibritogen C-terminal
; NAME/KEY: CARBOHYD
; LOCATION: (164)..(164)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
; NAME/KEY: CARBOHYD
; LOCATION: (192)..(192)
; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
US-09-983-000A-8

Query Match 99.9%; Score 2682; DB 10; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCVTCWMLGLILAMGAVAGQDGFEGTEGSPREFIYLNRYKRGESQDKCTYTFIV 60
DB 1 MRPLCVTCWMLGLILAMGAVAGQDGFEGTEGSPREFIYLNRYKRGESQDKCTYTFIV 60
QY 61 POORVTGALCVNSKEPEVLENNRVHAKQELINNELLNQKQIETLQOLVYVDGIVSEV 120
DB 61 POORVTGALCVNSKEPEVLENNRVHAKQELINNELLNQKQIETLQOLVYVDGIVSEV 120
QY 121 KILRKESRMNSRVQOLVYQOLLEHIIKRDNLLEISQLENRIINQADMLQASXYKDE 180

Db 121 KLRKESRNNNSRVTOYLMQLLHEIRKRDNALELSQLENRLINQADMLQASXYKDL 180
Qy 181 HKYQHLATLANHOSIITIAQLEEHQCRVPSARVPVPPPAAPRVYQPTNRIINQISTN 240
Db 181 HKYQHLATLANHOSIITIAQLEEHQCRVPSARVPVPPPAAPRVYQPTNRIINQISTN 240
Qy 241 EIOSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPMWDCQALDGHDTSSIVYKPEENTN 300
Db 241 EIOSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPMWDCQALDGHDTSSIVYKPEENTN 300
Qy 301 RLMQVWCQDQHDHDPGWTVIQRRLDGSVNFPRMNETYKQGFNIDGEYWLGLENIYWLTLNQ 360
Db 301 RLMQVWCQDQHDHDPGWTVIQRRLDGSVNFPRMNETYKQGFNIDGEYWLGLENIYWLTLNQ 360
Qy 361 GNYKLVMTMEDSGRKYFAEYASFRLEPSEYYKRLGRYHGNAGDSFTMHNGKQFTTLD 420
Db 361 GNYKLVMTMEDSGRKYFAEYASFRLEPSEYYKRLGRYHGNAGDSFTMHNGKQFTTLD 420
Qy 421 RDHDVYTGNCAYHOKGWMYNACAHSNLNGWYRGHYSRYODGVYMAEFRGGSYSLSKK 480
Db 421 RDHDVYTGNCAYHOKGWMYNACAHSNLNGWYRGHYSRYODGVYMAEFRGGSYSLSKK 480
Qy 481 VVMIRPNPNTFH 493
Db 481 VVMIRPNPNTFH 493

RESULT 4

US-10-147-493-268
; Sequence 268, Application US/10147493
; Publication No. US20040029217A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C345
; CURRENT APPLICATION NUMBER: US/10/147,493
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-147-493-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRPLCTCWMGLGLAAMGAVAGDEGFEETEGSPREFIYNRYKRGESQDKCTYTFIV 60
Db 1 MRPLCTCWMGLGLAAMGAVAGDEGFEETEGSPREFIYNRYKRGESQDKCTYTFIV 60
Qy 61 PQRVTGATCVNSKEPEVLLNRYKHQELINNELIKOKROIFTLQQLVYVDGIVSEV 120
Db 61 PQRVTGATCVNSKEPEVLLNRYKHQELINNELIKOKROIFTLQQLVYVDGIVSEV 120

Qy 121 KLRKESRNNNSRVTOYLMQLLHEIRKRDNALELSQLENRLINQADMLQASXYKDL 180
Db 121 KLRKESRNNNSRVTOYLMQLLHEIRKRDNALELSQLENRLINQADMLQASXYKDL 180
Qy 181 HKYQHLATLANHOSIITIAQLEEHQCRVPSARVPVPPPAAPRVYQPTNRIINQISTN 240
Db 181 HKYQHLATLANHOSIITIAQLEEHQCRVPSARVPVPPPAAPRVYQPTNRIINQISTN 240
Qy 241 EIOSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPMWDCQALDGHDTSSIVYKPEENTN 300
Db 241 EIOSDQNLKVLPPPLPTMPTLTSLPSSTDKPSGPMWDCQALDGHDTSSIVYKPEENTN 300
Qy 301 RLMQVWCQDQHDHDPGWTVIQRRLDGSVNFPRMNETYKQGFNIDGEYWLGLENIYWLTLNQ 360
Db 301 RLMQVWCQDQHDHDPGWTVIQRRLDGSVNFPRMNETYKQGFNIDGEYWLGLENIYWLTLNQ 360
Qy 361 GNYKLVMTMEDSGRKYFAEYASFRLEPSEYYKRLGRYHGNAGDSFTMHNGKQFTTLD 420
Db 361 GNYKLVMTMEDSGRKYFAEYASFRLEPSEYYKRLGRYHGNAGDSFTMHNGKQFTTLD 420
Qy 421 RDHDVYTGNCAYHOKGWMYNACAHSNLNGWYRGHYSRYODGVYMAEFRGGSYSLSKK 480
Db 421 RDHDVYTGNCAYHOKGWMYNACAHSNLNGWYRGHYSRYODGVYMAEFRGGSYSLSKK 480
Qy 481 VVMIRPNPNTFH 493
Db 481 VVMIRPNPNTFH 493

RESULT 5

US-10-145-127-268
; Sequence 268, Application US/10145127
; Publication No. US2004003558A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C252
; CURRENT APPLICATION NUMBER: US/10/145,127
; CURRENT FILING DATE: 2002-05-13
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-145-127-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRPLCTCWMGLGLAAMGAVAGDEGFEETEGSPREFIYNRYKRGESQDKCTYTFIV 60
Db 1 MRPLCTCWMGLGLAAMGAVAGDEGFEETEGSPREFIYNRYKRGESQDKCTYTFIV 60

QY 61 POORVTGAICVNSKEPEVLENNRVHKOELLENNELKKOKROJETLOOVKVDGIVSEV 120
DB 61 POORVTGAICVNSKEPEVLENNRVHKOELLENNELKKOKROJETLOOVKVDGIVSEV 120
QY 121 KILRKESRNNNSRVTOLYMQLLHEIRKDNALLESOLENRIINOTADMQLASKYKDE 180
DB 121 KILRKESRNNNSRVTOLYMQLLHEIRKDNALLESOLENRIINOTADMQLASKYKDE 180
QY 181 HKYOHATLANHOSSEIIAOLEEHCOVPSARVPVOPPPAAPPVOPPTYNRIINOISTN 240
DB 181 HKYOHATLANHOSSEIIAOLEEHCOVPSARVPVOPPPAAPPVOPPTYNRIINOISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSSTDKPSGPMWDCLOALBDGHTSSILYVKEBNTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSSTDKPSGPMWDCLOALBDGHTSSILYVKEBNTN 300
QY 301 RLMQWCDQHRDPGGMTVIOQLDGSVNFRRMWTYKQGFNGIDGYWLGLENITWLTNQ 360
DB 301 RLMQWCDQHRDPGGMTVIOQLDGSVNFRRMWTYKQGFNGIDGYWLGLENITWLTNQ 360
QY 361 GNYKLVTMEDWSGRKVFAEYASFRLPESEYKRLGRYHGNAGDSFTWNGKOPTTLD 420
DB 361 GNYKLVTMEDWSGRKVFAEYASFRLPESEYKRLGRYHGNAGDSFTWNGKOPTTLD 420
QY 421 RHDVYTGNCAYHOKGGMWYNACAHSNLNGWYRGSHYRSRYODGVYMAEFPGGSYSLKX 480
DB 421 RHDVYTGNCAYHOKGGMWYNACAHSNLNGWYRGSHYRSRYODGVYMAEFPGGSYSLKX 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

RESULT 6

US-10-160-503-268
; Sequence 268, Application US/10160503
; Publication No. US20040033559A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C46
; CURRENT APPLICATION NUMBER: US/10/160,503
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-160-503-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCYTCWMLGLLAAGVAGQEDGFEETGSGPREFTYLNRYKRAESODKCTYTFIV 60
|||||

DB 1 MRPLCYTCWMLGLLAAGVAGQEDGFEETGSGPREFTYLNRYKRAESODKCTYTFIV 60
QY 61 POORVTGAICVNSKEPEVLENNRVHKOELLENNELKKOKROJETLOOVKVDGIVSEV 120
DB 61 POORVTGAICVNSKEPEVLENNRVHKOELLENNELKKOKROJETLOOVKVDGIVSEV 120
QY 121 KILRKESRNNNSRVTOLYMQLLHEIRKDNALLESOLENRIINOTADMQLASKYKDE 180
DB 121 KILRKESRNNNSRVTOLYMQLLHEIRKDNALLESOLENRIINOTADMQLASKYKDE 180
QY 181 HKYOHATLANHOSSEIIAOLEEHCOVPSARVPVOPPPAAPPVOPPTYNRIINOISTN 240
DB 181 HKYOHATLANHOSSEIIAOLEEHCOVPSARVPVOPPPAAPPVOPPTYNRIINOISTN 240
QY 241 EIOSDONLKVLPPLPTMPTLTSLPSSTDKPSGPMWDCLOALBDGHTSSILYVKEBNTN 300
DB 241 EIOSDONLKVLPPLPTMPTLTSLPSSTDKPSGPMWDCLOALBDGHTSSILYVKEBNTN 300
QY 301 RLMQWCDQHRDPGGMTVIOQLDGSVNFRRMWTYKQGFNGIDGYWLGLENITWLTNQ 360
DB 301 RLMQWCDQHRDPGGMTVIOQLDGSVNFRRMWTYKQGFNGIDGYWLGLENITWLTNQ 360
QY 361 GNYKLVTMEDWSGRKVFAEYASFRLPESEYKRLGRYHGNAGDSFTWNGKOPTTLD 420
DB 361 GNYKLVTMEDWSGRKVFAEYASFRLPESEYKRLGRYHGNAGDSFTWNGKOPTTLD 420
QY 421 RHDVYTGNCAYHOKGGMWYNACAHSNLNGWYRGSHYRSRYODGVYMAEFPGGSYSLKX 480
DB 421 RHDVYTGNCAYHOKGGMWYNACAHSNLNGWYRGSHYRSRYODGVYMAEFPGGSYSLKX 480
QY 481 VMMIRPNPTFH 493
DB 481 VMMIRPNPTFH 493

RESULT 7

US-10-143-118-268
; Sequence 268, Application US/10143118
; Publication No. US2004003835A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C228
; CURRENT APPLICATION NUMBER: US/10/143,118
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-118-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVTCWMLGLIAAMGAVAGQEDGEGTSGSPREFIYLNRYKAGSODKCTYFTY 60
Db 1 MRPLVTCWMLGLIAAMGAVAGQEDGEGTSGSPREFIYLNRYKAGSODKCTYFTY 60
QY 61 POORVTGALCVNSKEPEVLLNRYVHKQELINNELLKQKQIETLQOLVKGAGSIVSEV 120
Db 61 POORVTGALCVNSKEPEVLLNRYVHKQELINNELLKQKQIETLQOLVKGAGSIVSEV 120
QY 121 KLLKRESRMNSRVTLQYMLLHEIIRKDNALISOLENRIINQADMLQASKYKXDL 180
Db 121 KLLKRESRMNSRVTLQYMLLHEIIRKDNALISOLENRIINQADMLQASKYKXDL 180
QY 181 HKYOHATLANQSEIITAOLEHQRVPSARPVPPAPAPRVYQPTYNRIINQISTN 240
Db 181 HKYOHATLANQSEIITAOLEHQRVPSARPVPPAPAPRVYQPTYNRIINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCLOALDGHDTSSIYLVKPENTN 300
Db 241 EIQSDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCLOALDGHDTSSIYLVKPENTN 300
QY 301 RLMQVWCDQHDHDPGQMTVIOIRLDGSVNFERNMETYKQGFNIDGEYWLGLENIYMLTNQ 360
Db 301 RLMQVWCDQHDHDPGQMTVIOIRLDGSVNFERNMETYKQGFNIDGEYWLGLENIYMLTNQ 360
QY 361 GNYKLLVTMEDWSGRKVFAYASFLPESEYYKLRGRHGNAGDSFTWNGKQFTLLD 420
Db 361 GNYKLLVTMEDWSGRKVFAYASFLPESEYYKLRGRHGNAGDSFTWNGKQFTLLD 420
QY 421 RDHDVYTGNCARHYQKGMWYNACAHSNLNGWYRGHYSRQDGYVMAEFPGSSYSLK 480
Db 421 RDHDVYTGNCARHYQKGMWYNACAHSNLNGWYRGHYSRQDGYVMAEFPGSSYSLK 480
QY 481 VVMIMIRPNENTFH 493
Db 481 VVMIMIRPNENTFH 493

RESULT 8
US-10-144-993-268
; Sequence 268, Application US/10144993
; Publication No. US20040038336A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C261
; CURRENT APPLICATION NUMBER: US/10/144,993
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRF
; ORGANISM: Homo Sapien
US-10-144-993-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPLVTCWMLGLIAAMGAVAGQEDGEGTSGSPREFIYLNRYKAGSODKCTYFTY 60
Db 1 MRPLVTCWMLGLIAAMGAVAGQEDGEGTSGSPREFIYLNRYKAGSODKCTYFTY 60
QY 61 POORVTGALCVNSKEPEVLLNRYVHKQELINNELLKQKQIETLQOLVKGAGSIVSEV 120
Db 61 POORVTGALCVNSKEPEVLLNRYVHKQELINNELLKQKQIETLQOLVKGAGSIVSEV 120
QY 121 KLLKRESRMNSRVTLQYMLLHEIIRKDNALISOLENRIINQADMLQASKYKXDL 180
Db 121 KLLKRESRMNSRVTLQYMLLHEIIRKDNALISOLENRIINQADMLQASKYKXDL 180
QY 181 HKYOHATLANQSEIITAOLEHQRVPSARPVPPAPAPRVYQPTYNRIINQISTN 240
Db 181 HKYOHATLANQSEIITAOLEHQRVPSARPVPPAPAPRVYQPTYNRIINQISTN 240
QY 241 EIQSDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCLOALDGHDTSSIYLVKPENTN 300
Db 241 EIQSDQNLKVLPPPLPTMPTLTSIPSSTDKPSGPMWDCLOALDGHDTSSIYLVKPENTN 300
QY 301 RLMQVWCDQHDHDPGQMTVIOIRLDGSVNFERNMETYKQGFNIDGEYWLGLENIYMLTNQ 360
Db 301 RLMQVWCDQHDHDPGQMTVIOIRLDGSVNFERNMETYKQGFNIDGEYWLGLENIYMLTNQ 360
QY 361 GNYKLLVTMEDWSGRKVFAYASFLPESEYYKLRGRHGNAGDSFTWNGKQFTLLD 420
Db 361 GNYKLLVTMEDWSGRKVFAYASFLPESEYYKLRGRHGNAGDSFTWNGKQFTLLD 420
QY 421 RDHDVYTGNCARHYQKGMWYNACAHSNLNGWYRGHYSRQDGYVMAEFPGSSYSLK 480
Db 421 RDHDVYTGNCARHYQKGMWYNACAHSNLNGWYRGHYSRQDGYVMAEFPGSSYSLK 480
QY 481 VVMIMIRPNENTFH 493
Db 481 VVMIMIRPNENTFH 493

RESULT 9
US-10-158-787-268
; Sequence 268, Application US/10158787
; Publication No. US20040039164A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C49
; CURRENT APPLICATION NUMBER: US/10/158,787
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 268
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapien
US-10-156-787-268

Query Match 99.9%; Score 2682; DB 12; Length 493;

Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAMGAVAGDEGEGTEGSPREFIYLRKVRAGSODKCTYTFIV 60
DB 1 MRPLCTCWMGLGLAMGAVAGDEGEGTEGSPREFIYLRKVRAGSODKCTYTFIV 60
QY 61 POORVTGALCVNSKEPEVLEENRVHKOBELELNNEILKOKROLETLOLVKVGIGVSEV 120
DB 61 POORVTGALCVNSKEPEVLEENRVHKOBELELNNEILKOKROLETLOLVKVGIGVSEV 120
QY 121 KILRKESRMNSRVTLQVQLHEITRKDNALIELSOLNRLINOTADMQLASKYKDE 180
DB 121 KILRKESRMNSRVTLQVQLHEITRKDNALIELSOLNRLINOTADMQLASKYKDE 180
QY 181 HKYCHLATTAAHNOSEIIAOLBEHCORVPSARVPPOPPAPRVVQPTYNRIINOISTN 240
DB 181 HKYCHLATTAAHNOSEIIAOLBEHCORVPSARVPPOPPAPRVVQPTYNRIINOISTN 240
QY 241 EIQSDONLKVLPPLPTMPTLTSLSSTDXKPSGPRDCLQALEDHDTSSIYLKVPENTN 300
DB 241 EIQSDONLKVLPPLPTMPTLTSLSSTDXKPSGPRDCLQALEDHDTSSIYLKVPENTN 300
QY 301 RLMQVWCDOHRDGGWTVIORLDSGVNFRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
DB 301 RLMQVWCDOHRDGGWTVIORLDSGVNFRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
QY 361 GNYKLLVTMEDSGKRVFAEYASFLRPESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLLVTMEDSGKRVFAEYASFLRPESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGCAHYQKGGWYNACAHSNLNGVYRGHYSRQODGYMAEFPGGSYSILK 480
DB 421 RDHDVYTGCAHYQKGGWYNACAHSNLNGVYRGHYSRQODGYMAEFPGGSYSILK 480
QY 481 VVMIRPNPTFH 493
DB 481 VVMIRPNPTFH 493

RESULT 10

US-10-140-024-268
Sequence 268, Application US/10140024
Publication No. US20040058424A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C69
CURRENT APPLICATION NUMBER: US/10/140,024
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 268
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-024-268

Query Match 99.9%; Score 2682; DB 12; Length 493;

Best Local Similarity 99.8%; Pred. No. 4,9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAMGAVAGDEGEGTEGSPREFIYLRKVRAGSODKCTYTFIV 60
DB 1 MRPLCTCWMGLGLAMGAVAGDEGEGTEGSPREFIYLRKVRAGSODKCTYTFIV 60
QY 61 POORVTGALCVNSKEPEVLEENRVHKOBELELNNEILKOKROLETLOLVKVGIGVSEV 120
DB 61 POORVTGALCVNSKEPEVLEENRVHKOBELELNNEILKOKROLETLOLVKVGIGVSEV 120
QY 121 KILRKESRMNSRVTLQVQLHEITRKDNALIELSOLNRLINOTADMQLASKYKDE 180
DB 121 KILRKESRMNSRVTLQVQLHEITRKDNALIELSOLNRLINOTADMQLASKYKDE 180
QY 181 HKYCHLATTAAHNOSEIIAOLBEHCORVPSARVPPOPPAPRVVQPTYNRIINOISTN 240
DB 181 HKYCHLATTAAHNOSEIIAOLBEHCORVPSARVPPOPPAPRVVQPTYNRIINOISTN 240
QY 241 EIQSDONLKVLPPLPTMPTLTSLSSTDXKPSGPRDCLQALEDHDTSSIYLKVPENTN 300
DB 241 EIQSDONLKVLPPLPTMPTLTSLSSTDXKPSGPRDCLQALEDHDTSSIYLKVPENTN 300
QY 301 RLMQVWCDOHRDGGWTVIORLDSGVNFRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
DB 301 RLMQVWCDOHRDGGWTVIORLDSGVNFRMWTYKOGFGNIDGYWLGLENIYWLINQ 360
QY 361 GNYKLLVTMEDSGKRVFAEYASFLRPESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
DB 361 GNYKLLVTMEDSGKRVFAEYASFLRPESEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGCAHYQKGGWYNACAHSNLNGVYRGHYSRQODGYMAEFPGGSYSILK 480
DB 421 RDHDVYTGCAHYQKGGWYNACAHSNLNGVYRGHYSRQODGYMAEFPGGSYSILK 480
QY 481 VVMIRPNPTFH 493
DB 481 VVMIRPNPTFH 493

RESULT 11

US-10-140-808-268
Sequence 268, Application US/10140808
Publication No. US20030017563A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C182
CURRENT FILING DATE: 2002-05-07
CURRENT APPLICATION NUMBER: US/10/140,808
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO: 268
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-808-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 1 MRPLCTTCWMLGILAMGAVAGDEGEGTEGSPREFIYLRKYRAGESQDKCTYTFIV 60
61 POORVTGATCVNSKEPEVLEENRVHKOELLNELLKOKROITLQOLVAVDGIYSEV 120
61 POORVTGATCVNSKEPEVLEENRVHKOELLNELLKOKROITLQOLVAVDGIYSEV 120
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
181 HKYOHATLANOSEIILAOLEHRCQVPSARPVQPPAPPRVYQPTYNRIINQISTN 240
181 HKYOHATLANOSEIILAOLEHRCQVPSARPVQPPAPPRVYQPTYNRIINQISTN 240
241 EIQSDNMLKVPPLPTMTLTSLPSTDKPSGPMWDCQALEDHGHTSSILVYKPENTN 300
241 EIQSDNMLKVPPLPTMTLTSLPSTDKPSGPMWDCQALEDHGHTSSILVYKPENTN 300
DB 301 RLMQVWCDDRHDPGQWTVIQRRLDGSVNFPRNMEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
301 RLMQVWCDDRHDPGQWTVIQRRLDGSVNFPRNMEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
361 GNYKLVTMEDWSGRKFAEYASFRLEPSEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
361 GNYKLVTMEDWSGRKFAEYASFRLEPSEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
DB 421 RDHDVYTGNCANHYQKGGWYNA CAHSNUNGVWYRGHYSRYQDGYVAEFGGSYSLSLK 480
421 RDHDVYTGNCANHYQKGGWYNA CAHSNUNGVWYRGHYSRYQDGYVAEFGGSYSLSLK 480
DB 481 VVMNIRPNPTTFH 493
481 VVMNIRPNPTTFH 493
DB 481 VVMNIRPNPTTFH 493
481 VVMNIRPNPTTFH 493

Publication No. US20030211571A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C383
CURRENT FILING DATE: 2002-05-20
CURRENT APPLICATION NUMBER: US/10/152,405
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO: 268
LENGTH: 493
TYPE: PRT
ORGANISM: Homo Sapien
US-10-152-405-268

Query Match 99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 1 MRPLCTTCWMLGILAMGAVAGDEGEGTEGSPREFIYLRKYRAGESQDKCTYTFIV 60
61 POORVTGATCVNSKEPEVLEENRVHKOELLNELLKOKROITLQOLVAVDGIYSEV 120
61 POORVTGATCVNSKEPEVLEENRVHKOELLNELLKOKROITLQOLVAVDGIYSEV 120
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
121 KILKRESNNNSRVTLQYLMOLHEIIRKDNALIELSOLERNILNQTDMLQLASKYKDL 180
181 HKYOHATLANOSEIILAOLEHRCQVPSARPVQPPAPPRVYQPTYNRIINQISTN 240
181 HKYOHATLANOSEIILAOLEHRCQVPSARPVQPPAPPRVYQPTYNRIINQISTN 240
241 EIQSDNMLKVPPLPTMTLTSLPSTDKPSGPMWDCQALEDHGHTSSILVYKPENTN 300
241 EIQSDNMLKVPPLPTMTLTSLPSTDKPSGPMWDCQALEDHGHTSSILVYKPENTN 300
DB 301 RLMQVWCDDRHDPGQWTVIQRRLDGSVNFPRNMEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
301 RLMQVWCDDRHDPGQWTVIQRRLDGSVNFPRNMEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
361 GNYKLVTMEDWSGRKFAEYASFRLEPSEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
361 GNYKLVTMEDWSGRKFAEYASFRLEPSEYKRLGRYHGNAGDSFTWHNGQFTTLD 420
DB 421 RDHDVYTGNCANHYQKGGWYNA CAHSNUNGVWYRGHYSRYQDGYVAEFGGSYSLSLK 480
421 RDHDVYTGNCANHYQKGGWYNA CAHSNUNGVWYRGHYSRYQDGYVAEFGGSYSLSLK 480
DB 481 VVMNIRPNPTTFH 493
481 VVMNIRPNPTTFH 493
DB 481 VVMNIRPNPTTFH 493
481 VVMNIRPNPTTFH 493

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RESULT 13
US-10-127-852A-268
; Sequence 268, Application US/10127852A
; Publication No. US20030203428A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C88
; CURRENT APPLICATION NUMBER: US/10/127,852A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-127-852A-268

Query Match          99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4, 9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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; DB 181 HKYOHATLAHNOSEIIAQLSEHCORVPSARVPVPPAPAPRVYQPTVNRRIINOISTN 240
; QY 241 EIOSDQNLKYLPPPLPTMTPLTSLPSSTDKPSGPMWDCLOALBDGHTSISYLVKPEENTN 300
; DB 241 EIOSDQNLKYLPPPLPTMTPLTSLPSSTDKPSGPMWDCLOALBDGHTSISYLVKPEENTN 300
; QY 301 RLMOVWCDQHRDPGQWTVIOIRLDGSVNFRRMETTKQGFNGINDSEYVIGLENTIYMLTNO 360
; DB 301 RLMOVWCDQHRDPGQWTVIOIRLDGSVNFRRMETTKQGFNGINDSEYVIGLENTIYMLTNO 360
; QY 361 GNYGLVLTMDMSGRKFAYEASFRLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
; DB 361 GNYGLVLTMDMSGRKFAYEASFRLPESEYYKLRGRYHGNAGDSFTWNGKQFTTLD 420
; QY 421 RDEHVTGNCAHYQKGGWYNACASHNLNGVYRGHYRSRYODGYVMAEFRCGSYSLKX 480
; DB 421 RDEHVTGNCAHYQKGGWYNACASHNLNGVYRGHYRSRYODGYVMAEFRCGSYSLKX 480
; QY 481 VVMWIRPNPTFH 493
; DB 481 VVMWIRPNPTFH 493

RESULT 14
US-10-127-900A-268
; Sequence 268, Application US/10127900A
; Publication No. US20030203428A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C81
; CURRENT APPLICATION NUMBER: US/10/127,900A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268

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; LENGTH: 493
; TYPE: PR
; ORGANISM: Homo Sapien
US-10-127-900A-268

Query Match      99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAANGAVAGDEGEGTEGSPREFIYLNRYKRAGESODKCTYTFIV 60
DB 1 MRPLCTCWMGLGLAANGAVAGDEGEGTEGSPREFIYLNRYKRAGESODKCTYTFIV 60
QY 61 POORVTGAI CVNSKEPEVLL ENRVAKOELINNELLKOKROJETTLOQLVKGIVSEV 120
DB 61 POORVTGAI CVNSKEPEVLL ENRVAKOELINNELLKOKROJETTLOQLVKGIVSEV 120
QY 121 KLLRKESRRNNSRVYQLYMOQLHEIIRKDNAL ELSOLENRLINQADMLQASKYKOLE 180
DB 121 KLLRKESRRNNSRVYQLYMOQLHEIIRKDNAL ELSOLENRLINQADMLQASKYKOLE 180
QY 181 HKYOH LATAHNOSEIIAOLEEHCORVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
DB 181 HKYOH LATAHNOSEIIAOLEEHCORVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
QY 241 EIQSDQNLKVLPPPLPTMTLTSLPSSTDKPSGPMRDCLQALBDGHDTSIYLVKPENTN 300
DB 241 EIQSDQNLKVLPPPLPTMTLTSLPSSTDKPSGPMRDCLQALBDGHDTSIYLVKPENTN 300
QY 301 RLMQWVCDQRHDPGGWTVIQRLDGSVNFPRMNETYKQSGFNI DGEIYWLGL ENIYWLNO 360
DB 301 RLMQWVCDQRHDPGGWTVIQRLDGSVNFPRMNETYKQSGFNI DGEIYWLGL ENIYWLNO 360
QY 361 GNYKLVLT MEDWSGRKFAEYASFRLEPSEYYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
DB 361 GNYKLVLT MEDWSGRKFAEYASFRLEPSEYYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
QY 421 RHDVYTGNCAYKQKGWMTNACAHSNLNGWYRGHYSRKYODGYVAEFRGGSYSLLK 480
DB 421 RHDVYTGNCAYKQKGWMTNACAHSNLNGWYRGHYSRKYODGYVAEFRGGSYSLLK 480
QY 481 VMMIRPNPNTFH 493
DB 481 VMMIRPNPNTFH 493

RESULT 15
US-10-128-685A-268
; Sequence 268, Application US/10128685A
; Publication No. US20030203430A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C116
; CURRENT APPLICATION NUMBER: US/10/128,685A
; CURRENT FILING DATE: 2002-04-23
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; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 268
; LENGTH: 493
; TYPE: PR
; ORGANISM: Homo Sapien
US-10-128-685A-268
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Query Match      99.9%; Score 2682; DB 12; Length 493;
Best Local Similarity 99.8%; Pred. No. 4.9e-210;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLCTCWMGLGLAANGAVAGDEGEGTEGSPREFIYLNRYKRAGESODKCTYTFIV 60
DB 1 MRPLCTCWMGLGLAANGAVAGDEGEGTEGSPREFIYLNRYKRAGESODKCTYTFIV 60
QY 61 POORVTGAI CVNSKEPEVLL ENRVAKOELINNELLKOKROJETTLOQLVKGIVSEV 120
DB 61 POORVTGAI CVNSKEPEVLL ENRVAKOELINNELLKOKROJETTLOQLVKGIVSEV 120
QY 121 KLLRKESRRNNSRVYQLYMOQLHEIIRKDNAL ELSOLENRLINQADMLQASKYKOLE 180
DB 121 KLLRKESRRNNSRVYQLYMOQLHEIIRKDNAL ELSOLENRLINQADMLQASKYKOLE 180
QY 181 HKYOH LATAHNOSEIIAOLEEHCORVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
DB 181 HKYOH LATAHNOSEIIAOLEEHCORVPSARVPPOPPAPPRVYQPTYNRIINOISTN 240
QY 241 EIQSDQNLKVLPPPLPTMTLTSLPSSTDKPSGPMRDCLQALBDGHDTSIYLVKPENTN 300
DB 241 EIQSDQNLKVLPPPLPTMTLTSLPSSTDKPSGPMRDCLQALBDGHDTSIYLVKPENTN 300
QY 301 RLMQWVCDQRHDPGGWTVIQRLDGSVNFPRMNETYKQSGFNI DGEIYWLGL ENIYWLNO 360
DB 301 RLMQWVCDQRHDPGGWTVIQRLDGSVNFPRMNETYKQSGFNI DGEIYWLGL ENIYWLNO 360
QY 361 GNYKLVLT MEDWSGRKFAEYASFRLEPSEYYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
DB 361 GNYKLVLT MEDWSGRKFAEYASFRLEPSEYYKRLGRYHGNAGDSFTWHNGKQFTTLD 420
QY 421 RHDVYTGNCAYKQKGWMTNACAHSNLNGWYRGHYSRKYODGYVAEFRGGSYSLLK 480
DB 421 RHDVYTGNCAYKQKGWMTNACAHSNLNGWYRGHYSRKYODGYVAEFRGGSYSLLK 480
QY 481 VMMIRPNPNTFH 493
DB 481 VMMIRPNPNTFH 493
```

Search completed: July 30, 2004, 12:43:16
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2004, 12:32:34 ; Search time 18 seconds
(without alignments)
2634.579 Million cell updates/sec

Title: US-10-018-386-2

Perfect score: 2686

Sequence: 1 MRPLCTCMTGLTAAAGAV.....GSYSIKVVMIRNPNTFH 493

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 78: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533	19.8	312	2 JN0596	fibrinogen-related
2	526.5	19.6	491	1 FGHUB	fibrinogen beta ch
3	524.5	19.5	468	1 FGBOB	fibrinogen beta ch
4	520.5	19.4	866	2 D44234	fibrinogen alpha c
5	512.5	19.1	479	2 A25052	fibrinogen beta ch
6	503	18.7	463	2 A38463	fibrinogen beta ch
7	501	18.7	437	1 FGHUG	fibrinogen gamma-A
8	501	18.7	453	1 FGHUB	fibrinogen gamma-B
9	500	18.6	328	2 A05299	fibrinogen beta ch
10	485	18.4	282	2 A35084	fibrinogen-related
11	489.5	18.2	438	2 A32670	fibrinogen gamma c
12	488	18.2	1356	2 A45445	jannuin precursor,
13	484.5	18.0	326	2 B47172	fibrin-beta - pig
14	483.5	18.0	326	2 S61517	fibrinogen-1 precursor
15	483.5	18.0	432	2 A27447	cytotoxic T-lympho
16	483.5	18.0	323	2 A47172	transforming growt
17	482.5	18.0	334	2 UCS580	fibrin-A precursor
18	480.5	17.9	439	2 I37391	fibrinogen-like pr
19	480.5	17.9	1353	1 JH0675	restrictin precurs
20	479.5	17.9	432	2 I56934	fibrinogen-like pr
21	476.5	17.7	444	2 S05133	fibrinogen gamma-B
22	465.5	17.3	641	2 A41932	fibrinogen alpha-I
23	463.5	17.3	432	1 FGLMG	fibrinogen gamma c
24	459	17.1	437	1 FGRGA	fibrinogen gamma-A
25	459	17.1	445	1 FGRGB	fibrinogen gamma-B
26	455.5	17.0	417	2 S65944	tenascin-X - pig (
27	452	16.8	860	2 I48839	tenascin-X - mouse
28	451.5	16.8	3566	1 A40701	tenascin-X precurs
29	451.5	16.8	4135	2 T42629	tenascin-X - bovin

30	450.5	16.8	1810	1 A32230	tenascin precursor
31	448	16.7	4006	2 T09070	probbble tenascin
32	444.5	16.5	220	2 S28170	tenascin homolog -
33	444.5	16.2	1746	1 S19694	tenascin precursor
34	423.5	15.8	2019	1 J01322	tenascin precursor
35	421.5	15.7	2201	2 A32160	tenascin-C - human
36	381.5	14.6	1914	2 T42635	tenascin Y precurs
37	388.5	14.5	774	2 A39832	scabrous locus (sc
38	257.5	9.6	463	2 T15876	hypothetical prote
39	235.5	8.8	127	2 PC2036	microfibril-associ
40	188.5	7.0	431	2 T29680	hypothetical prote
41	174	6.5	452	2 T26827	hypothetical prote
42	172.5	6.4	933	2 A31930	cytoactin - chick
43	156.5	5.8	77	2 I51647	tenascin - African
44	155	5.8	146	2 T32255	hypothetical prote
45	153	5.7	744	2 F95013	pneumococcal surfa

ALIGNMENTS

RESULT 1

JN0596 fibrinogen-related protein HFRP-1 precursor - human

C:Species: Homo sapiens (man)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000

C:Accession: JN0596

R:Yamamoto, T.; Gotoh, M.; Sasaki, H.; Terada, M.; Kiteajima, M.; Hirohashi, S.

R:Biochem. Biophys. Res. Commun. 193, 661-687, 1993

A:Title: Molecular cloning and initial characterization of a novel fibrinogen-related ge

A:Reference number: JN0596; MUID:33290661; PMID:8390249

A:Accession: JN0596

A:Molecule type: mRNA

A:Residues: 1-312 <YAM>

A:Cross-references: GS:D1446; NID:G393314; PIDN:BA0336.1; PID:G393315

A:Experimental source: liver

C:Superfamily: fibrinogen beta/gamma homology

F.1-17/Domain: signal sequence #status predicted <SIG>

F.18-312/Product: fibrinogen-related protein HFRP-1 #status predicted <MAT>

F.80-305/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 19.8%; Score 533; DB 2; Length 312;
Best local similarity 39.3%; Pred. No. 1.9e-27;
Matches 110; Conservative 41; Mismatches 89; Indels 40; Gaps 9;

QY	232	RIINGISTNEIQ----	SDPNKIVPPLPTMTLS	PSSTDKPSGPRDCLQALDQHD	287
DB	50	KIKQLQENEVQFLDKGDED-----	TVVDLSKRGQ-----	YADSEIFNDGYK	92
QY	288	TSIYLVPENTNRLTMQWCDQRHDPGQWTVIQR	LDGSVNFNNMETTYKGFQNI---D	344	
DB	93	LSGFYKIKFQSPAEFSYCDM--SDGGWTVIQ	RRSGSENFNGMXDYENGFNFYQKH	151	
QY	345	GEYHIGLENTWLNQGYKLLVMEDESKGKVA	EAFLESESEYKRLRYGNA	404	
DB	152	GEYWGKNKHLFTQEDYTLKIDLADEKNSRA	QYKVFYGEKXFEIANTIEFGTA	211	
QY	405	GDSEFT-----W--HNGKQFTLLDRHDV	TYGNCAPHYQGGWYNAAASHNLNGVY	453	
DB	212	GDSLAGNFHPEVQWASHQRMKFTWDRDHDN	YDGNCAEFDQSGWMEFNRCHSANTLNGVY	271	
QY	454	RGRHRSRYQDGVVAERFGSGYSILKYVMIR	PN---PN	490	
DB	272	SGPYTAKTDNGIWTYTHGWMYSLKSVMKIR	PNDFIPN	310	

RESULT 2

FGHUB fibrinogen beta chain precursor [validated] - human
N:Alternate names: coagulation factor I
N:Contains: fibrinopeptide B
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 31-Mar-1993 #text_change 08-Dec-2000


```

Db      272  MNTENGWTVLQNRDGGVDFGRKMDPYKQGFNATVTDKNTYCGLEGEYTLANDKTSQ 331
      357  LTNOGNKYLVTWEMSGRKYVAEYASFLPESEYYKLRLGRYAGNAGD----- 406
      332  LTRMGPTTELLIEMEMKEDKVAHGYGFTVQNEANKYQISVNRKGTGNAIIMGASQIM 391
      407  ----SFTWNGKQFTLLDRHDVYTG-----CAHYQKGGWYVNAQAHNINGVWYRGCH 457
      392  GENRTMTLHNGWFFSTYDRDNDGMLTSPRKQCSKEDGGWYVNRCHANNENGRYWGQ 451
      458  Y-----RSRYQDGYVVAEFRGGSYSLKXVVMIRP 487
      452  YTWMAKHGTDDPGVVMNMKSGWSYMRKMSKIRP 486

```

RESULT 3

R:BOB

fibrinogen beta chain - bovine

N:Contains: fibrinopeptide B

C:Species: Bos primigenius taurus (cattle)

C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 13-Sep-1996

A:Accession: A03112; B03117; B37507; A37513; S02443

R:Blomback, B.; Doellittle, R.F.

Acta Chem. Scand. 17, 1816-1819, 1963

A>Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.

A:Reference number: A03122

A:Accession: A03122

A:Molecule type: protein

A:Residues: 1-4 <BLO>

R:Stojaniet, J.; Blomback, B.; Wallen, P.

Ark. Kent. 16, 425-436, 1960

A>Title: Amino acid sequence of bovine fibrinopeptides.

A:Reference number: A03117

A:Accession: B03117

A:Molecule type: protein

A:Residues: 5-21 <SUC>

R:Marinelli, R.A.; Inglis, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.

Arch. Biochem. Biophys. 192, 27-32, 1979

A>Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin

A:Reference number: A37507; MUID:79164394; PMID:434821

A:Accession: B37507

A:Molecule type: protein

A:Residues: 22-53 <WAR>

R:Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981

A>Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen

A:Reference number: A37513; MUID:81199473; PMID:6262803

A:Accession: A37513

A:Molecule type: mRNA

A:Residues: 44-468 <CHU>

R:Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.

FEBS Lett. 232, 56-60, 1988

A>Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to

A:Reference number: S02443; MUID:8821875; PMID:296748

A:Accession: S02443

A:Molecule type: protein

A:Residues: 373-374 <MED>

C:Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide

C:Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

C:Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoliprotein

F:76-205/Domain: fibrinogen disulfide ring homology <FDR>

F:215-464/Domain: fibrinogen beta/gamma homology <FBG>

F:1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

F:6/Binding site: sulfate (Tyr) (covalent) #status experimental

F:21-22/Cleavage site: Arg-Gly (thrombin) #status experimental

F:31/Binding site: carboxylate (Asn) (covalent) #status predicted

F:372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 19.5%; Score 524.5; DB 1; Length 468;

Best Local Similarity 30.3%; Pred. No. 1.2e-26;

Matches 134; Conservative 69; Mismatches 126; Indels 113; Gaps 12;

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      92  LNNELLKQK-----QIETLQQLVKGDIYSEVYKLRKSRNNNSRYTQYMLHEIR 147
      89  LQDTLVROEERPIKRSIEDLNTV-----DSVSTSSSTQYITLLNNMK 133
      148  KEDNALELSQENRILNQADMLQASKYDLEHKYQHLATLHANQSEIIAQLEHCORV 207
      134  GRQNV-----QDNENVNVEYSHLEKQLYTD-----ETVKN----- 167
      208  PSARVPVQPPAAPPRVYQPPYRILINQISTN-----ETQSDQNLKLPPLPTMPTL 261
      168  -----IPTKLRLVRSILENIRSKIOCLESDVSTQMEYCRTPCTVT- 207
      262  TSLPSSITDKRSQWRDCLQALEDHQPSISYLVKPEVNTNVMQWCDQRPDGMVYQR 321
      208  CNLPVYSGK-----ECKLIRNEGTSYMTLQPEDSSKPYRYVYCDMKTEKGMVYQN 261
      322  RLDSVNFPPNWTETKQGFNI-----DGEYTLGLENIYVLTNQGNYKLLVTM 369
      262  RQDSGLDFGRKMDPYKQGFNATVNAEGKKYCGVPGEYWLGNDRISQITWNGPTKLLIEM 321
      370  EDMSGKRVFAPYASFLPESEYYKLRLGRYAGNAGD-----SFTWNGKQ 415
      322  EDWKGDKVTLALYEGFTVQNEANKYQLSVSKYKGTAGNALIEGASQLVGENRTMTLHNSMF 381
      416  FTTLDPRHDVY-----TGNCAHYQKGGWYVNAQAHNINGVWYRGCHY-----RSRYQDG 465
      382  FSTYDRDNDGKTTDPRKQCSKEDGGWYVNRCHANNENGRYWGAYTWMMAKHGTDDG 441
      466  YVMAEPRGGSYSLKXVVMIRP 487
      442  VVMNMQSGWSYMRKMSKIRP 463

```

RESULT 4

fibrinogen alpha chain precursor, extended splice form - human

N:Alternate names: coagulation factor I

N:Contains: fibrinopeptide A

C:Species: Homo sapiens (man)

C:Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001

A:Accession: B44234; B44234

R:Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma

Biochemistry 31, 11968-11972, 1992

A>Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a novel

A:Reference number: A44234; MUID:93090725; PMID:1457396

A:Accession: D44234

A:Molecule type: protein

A:Residues: 1-866 <FU>

A:Cross-references: GB:M58569; NID:G182406; PID:G182407

A:Note: neither the complete nucleic acid sequence nor the complete translation are shown

A:Accession: B44234

A:Molecule type: mRNA; DNA

A:Residues: 605-866 <FU2>

A:Note: sequence extracted from NCBI backbone (NCBI:119917)

C:Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.

C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave

C:Comment: sites responsible for the formation of the soft clot.

C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz

C:Comment: ger) and between alpha chains (weaker) of different monomers.

C:Comment: All fibrinogen chains are synthesized in the liver.

C:Comment: See PIR:FGHVA for the major splice form. It is not known whether this form is

C:Genetics: GDB:FGA

A:Cross-references: GDB:119129; OMIM:134820

A:Map position: 4q28-4q28

A:Introns: 18/3; 60/3; 122/1; 171/2

A:Note: the list of introns is incomplete

C:Complex: the fibrinogen molecule is a hexamer containing two sets of three nonidentical

C:Function: the fibrinogen molecule is a hexamer containing two sets of three nonidentical

C:Function: the fibrinogen molecule is a hexamer containing two sets of three nonidentical

C:Function: the fibrinogen molecule is a hexamer containing two sets of three nonidentical

A,Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A,Pathway: blood coagulation
C,Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C,Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F,119/Domain: signal sequence #status predicted <SIG>
F,20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F,20-863/Product: fibrinopeptide A #status experimental <APT>
F,36-863/Product: fibrin alpha chain, extended splice form #status predicted <FCA>
F,57/Domain: fibrinogen disulfide ring homology <FDR>
F,591-593/Region: cell attachment (R-G-D) motif
F,629-663/Domain: fibrinogen beta/gamma homology <FBG>
F,32/460/Binding site: phosphate (Ser) (covalent) #status experimental
F,32/460/Binding site: Arg-Gly (thrombin) #status experimental
F,47/Disulfide bonds: interchain (to alpha-47) #status experimental
F,55/Disulfide bonds: interchain (to beta-95) #status experimental
F,64/Disulfide bonds: interchain (to gamma-49) #status experimental
F,160/Disulfide bonds: interchain (to beta-106) #status experimental
F,144/Disulfide bonds: interchain (to beta-223) #status experimental
F,288-419/Binding site: carbohydrate (Asn) (covalent) #status absent
F,322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F,347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F,461-491/Disulfide bonds: #status experimental
F,527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
F,686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 520.5; DB 2; Length 866;
Best Local Similarity 43.3%; Pred. No. 4.9e-26;
Matches 104; Conservative 40; Mismatches 69; Indels 27; Gaps 7;

272 SGFWRC---LQALDEGHTSSIVLVKPNTRLMQWCDQRHDPGWTIQRLDGSVN 328
Db SRVRCDDVLQHPFG--TQSGFNKLFSSKISFVYDQDTSLGMLTIQRRDGLN 684
QY 329 FFRNMTYKQGRNT---DGEVJGLENIYWLTVNQGNYKLLVTVMEDSGRRVFAEYASF 384
Db 685 FRTWQDYKRGKGLSDEBEGFWLGNLYLTLTGKSV--LRVELDAGNEAYEY--HF 742
QY 385 RLEPESEYKLRIGRHYNAGDS-----FTWNGKQFTLLDHPDYVTCNGHY 433
Db 743 RVGSEHAGALQVSSYEGTAGDALLRGSVEGAEVTSNNMOFSTFDADADWENCAEV 802
QY 434 QKGGWYNAKAHNSNNGWYRGHYR---YODGYVAEFGGYSYLKRYVMIRP 487
Db 803 YGGGWYNNCAANLNGIYYPGGSYDPRNNSPYEENGWVWSPFGADYSLRAVAKIRP 862

RESULT 5

A25052
Fibrinogen beta chain - sea lamprey (fragments)
N,Contains: fibrinopeptide B
C,Species: Petromyzon marinus (sea lamprey)
C,Date: 25-Oct-1987 #sequence revision 19-Feb-1999 #text_change 13-Aug-1999
A,Accession: A25052; E03124; E03124
R,Bohmer, V.L.; Deolittle, R.F.; Pontes, M.; Strong, D.D.
Biochemistry 25, 6512-6516, 1986
A,Title: Complementary DNA sequence of lamprey fibrinogen beta chain.
A,Reference number: A25052; MUID:87076582; PMID:3790537
A,Accession: A25052
A,Molecule type: mRNA
A,Residues: 39-479 <BOH>
A,Cross-references: GB:M4773; NID:9213191; PIDN:AAA49261.1; PID:G213192
R,Cottrill, B.A.; Deolittle, R.F.
Biochem. Biophys. Acta 453, 426-438, 1976
A,Title: Amino acid sequences of lamprey fibrinopeptides A and B and characterization of
A,Reference number: A03120; MUID:77065679; PMID:999898
A,Accession: A03124
A,Molecule type: protein
A,Residues: 1-36 <COT1>
A,Accession: B03124
A,Molecule type: protein
A,Residues: 37-42 <COT2>
C,Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

C,Keywords: blood coagulation; glycoprotein; sulforprotein
F,11-36/Product: fibrinopeptide B #status experimental <FBP>
F,37-479/Product: fibrin beta chain #status experimental <MAT>
F,90-219/Domain: fibrinogen disulfide ring homology <FDR>
F,229-477/Domain: fibrinogen beta/gamma homology <FBG>
F,113/Binding site: sulfate (Tyr) (covalent) #status experimental
F,127/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.1%; Score 512.5; DB 2; Length 479;
Best Local Similarity 29.2%; Pred. No. 7.2e-26;
Matches 136; Conservative 64; Mismatches 136; Indels 128; Gaps 15;

QY 67 GATVNSKE-PEVLNLR-----YHKELELNNELIKQKQIETLQOLVYKVGIV 117
Db 94 GVLPTGCELRBELKQRPVRYKISMLKQNTLYFNSFDRMADSNTLTKQ----- 144
QY 118 SEVLTKRESNNRNVYQOLYHRIIRKQNALESLQENRILNQTADMQLASKYK 177
Db 145 -NVQTLK---RANRSRS-----THVNAOK-----EENR-----YK 172
QY 178 DLEHKYQH-LATLAHNSQETIAQLEHQQRPAPRPVPPAPRPVYQPTFYRIHQ 236
Db 173 EVKIRISTVAGSIRSKSVLEHLRAQMGREAIKQKELCSAPCTV----- 220
QY 237 ISTNEISDQNLKVLPPPLPTMPTLNSPSTKPGGPRDCQALDEGHTSIYLVK 296
Db 221 -----NCRV-----PVSQM-----HCDIYRNGRTSEAYYIDP 250
QY 297 ENTNRLMQWCDQRHDPGWTIQRLDGSVNFPRNMTYKQFG-----NIDG 345
Db 251 DLSEBPYKVCDESHGGGWTQVQNVDSNSNFAFMNTYKAFGNARNGKSGICNIG 310
QY 346 EYVLGLENIYWLTVNQGNYKLLVTVMEDSGRRVFAEYASFLEPESEYKLRIGRHYNAG 405
Db 311 EYVLGTVYQALTKQHTQVQLFPMSSDEGSSVYAQVAFRPEEAGQRYLWEDVYSGNAG 370
QY 406 D-----FTWNGKQFTLLDHPDYV-----TGCAHYQKGGWYNAKAS 446
Db 371 NALLEGATQMGKRNRTITNGQFSTFDRNDNNMPPGPTKCSDEPAGWYRNCHAA 430
QY 447 NLNGWYRGHYR---YODGYVAEFGGYSYLKRYVMIRP 487
Db 431 NPNGRVYMGGIYTKQADYDGDGVVWNNWKGSMYMEQWAMKLRP 476

RESULT 6

A38463
Fibrinogen beta chain - chicken (fragment)
C,Species: Gallus gallus (chicken)
C,Date: 31-Jul-1991 #sequence revision 31-Jul-1991 #text_change 13-Aug-1999
A,Accession: A38463
R,Meisbach, L.; Oddoux, C.; Procyk, R.; Gieninger, G.
Biochemistry 30, 3290-3294, 1991
A,Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
A,Reference number: A38463; MUID:91182745; PMID:2009266
A,Accession: A38463
A,Molecule type: mRNA
A,Residues: 1-463 <MEI>
A,Cross-references: GB:M5614; NID:9211779; PIDN:AAA48770.1; PID:9211780
C,Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
F,73-202/Domain: fibrinogen disulfide ring homology <FDR>
F,212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.7%; Score 503; DB 2; Length 463;
Best Local Similarity 29.6%; Pred. No. 2.9e-25;
Matches 128; Conservative 63; Mismatches 146; Indels 96; Gaps 11;
QY 92 LNNELIKQKQIETLQOLVYKVGIVSEYKLRKESNNRNVYQOLYHRIIRKDN 151
Db 86 LQTTLLKQKQKTVYLRDLK-----DRVAKFSSTSTMYQYVNMIDNLTQVTKQKRDN 139
QY 152 ALELSQLENRILNQTADMQLASKYKDEHKYQH-LATLAHNSQETIAQLEHQQRPAPR 211


```

Db      140 DILISEYNT-----EMELHYNKYKMDND-----NIPSSL 169
Qy      212 FVPQPPAPAPRVVQPTNYRINQISNTEIOSDONLAVLPPLPTWPTLTSLP--SSSTD 269
Db      170 RV-----LRAVIDSLH-KKIOKLEN-----AATQTDYGRSPCVASCN 206
Qy      270 KPSGWRDCLQLEDGHHTSSLYLVKPEPNTNLMQVCDQRHDPGQWTVIGPRIDGSVNF 329
Db      207 IPVSGRECEDEYRKQGETSEMYTIQDPFTTPYAVYCDMETDNGMTLIONRODGSVNF 266
Qy      330 FRNMETVQGFNT-----DGEVYLGLENIVYLTQNGNKLVTMEDNSGRVVF 378
Db      267 GQAMDEYKRGFGFNIAKSGGKRYCDTPGEVYLGNDKISQLTGPTKVLIEEDMNGDVS 326
Qy      379 AEVASFRLPESESEYKYLRLGRYHGNACD-----SFTWNGKQPTLLDRDHD 424
Db      327 ALYGFETTHNEGKXQOLSVNKGNAAGNALMGASQLVGENRTWTITHHNGVFSTYDRND 386
Qy      425 VT-----TGNCAHYKQKGMWYNACASNSLNGVWTRGHI-----RSRQDGYVAEPRGG 474
Db      387 GMLTTDPRKQCKEDGGGGMWYRCHAAVNGRYWGTYSDMAKHGTDDGIVWNNWEGS 446
Qy      475 SYSLKVVWVWIRP 487
Db      447 WYSMKKMKIKP 459

```

RESULT 7

FCHUG

fibrinogen gamma-A chain precursor [validated] - human

AltName: Homo sapiens (man)

CDate: 24-Apr-1984 #sequence revision 25-Feb-1985 #text change 08-Dec-2000

CAccession: A90470; B90494; C94433; B92448; I37393; A40698; H54223; A03125; C37

R.Chung, D.W.; Chan, W.Y.; Davie, E.W.

Biochemistry 22, 3250-3256, 1983

A>Title: Characterization of a complementary deoxyribonucleic acid coding for the gamma

A:Reference number: A90470; MUID:83283434; PMID:6688357

A:Accession: A90470

A:Molecule type: mRNA

A:Residues: 1-437 <CHU>

R.Rixon, M.W.; Chung, D.W.; Davie, E.W.

Biochemistry 24, 2077-2086, 1985

A>Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.

A:Reference number: A90494; MUID:85252774; PMID:2390550

A:Accession: B90494

A:Molecule type: DNA

A:Residues: 1-113, '1', '115-437 <RIX>

A:Cross-references: GB:X02415; GB:M00014; NID:G182438; PIDN:AB59531.1; PID:G182439

R.Henschen, A.; Lottepeich, F.; Southan, C.; Topfer-Petersen, E.

In Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe

A>Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v

A:Reference number: A94433

A:Accession: C94433

A:Molecule type: protein

A:Residues: 27-437 <HEN>

R.Kant, J.A.; Lord, S.T.; Crabtree, G.R.

Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983

A>Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: ev

A:Reference number: A93956; MUID:83247396; PMID:6575389

A:Accession: B93956

A:Molecule type: mRNA

A:Residues: 276-437 <KAN>

R.Fornace Jr., A.J.; Cummings, D.E.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.

J. Biol. Chem. 259, 12826-12830, 1984

A>Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the

A:Reference number: A92448; MUID:85030379; PMID:6092346

A:Accession: B92448

A:Molecule type: DNA

A:Residues: 286-437 <FOR>

R.Tam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.

Nucleic Acids Res. 11, 7427-7434, 1983

A>Title: Isolation and characterization of cDNA clones for the Alpha- and gamma-chains

A:Reference number: I37393; MUID:84069777; PMID:6689067

A:Accession: I37393

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 209-270 <RES>

A:Cross-references: EMBL:X00086; NID:G31445; PIDN:CAA24944.1; PID:9577055

R.Bertagnoli, M.S.; Beckert, W.C.

J. Cell Biol. 121, 1329-1342, 1993

A>Title: Evidence for the selective association of a subpopulation of GPIIb-IIIa with th

A:Reference number: A40698; MUID:93286185; PMID:8509453

A:Accession: A40698

A:Molecule type: protein

A:Residues: 27-33, 'XX', '36-41 <BER>

A:Experimental source: thrombin-activated platelets

A>Note: sequence extracted from NCBI backbone (NCBIP:13734)

R.Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.

Biochemistry 33, 1988-1993, 1994

A>Title: Identification of proteins associated with apolipoprotein A-I-containing lipop

A:Reference number: A54223; MUID:94162201; PMID:8117655

A:Accession: H54223

A:Molecule type: protein

A:Residues: 27-33, 'XX', '36-41 <KUN>

A>Note: identification of tryptic peptides from high-density lipoproteins

R.Henschen, A.; Lottepeich, F.; Kehl, M.; Southan, C.

Ann. N. Y. Acad. Sci. 408, 28-43, 1983

A>Title: Covalent structure of fibrinogen.

A:Reference number: A90037; MUID:83254370; PMID:6575669

A:Contents: annotation; review, disulfide bonds

R.Doolittle, R.F.; Takagi, T.; Walt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; G

In Regulatory Proteolytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt

A>Title: The structures of fibrinogen and fibrin.

A:Reference number: A94437

A:Contents: annotation; disulfide bonds

R.Blomback, B.; Hessel, B.; Hogg, D.

Thromb. Res. 9, 639-658, 1976

A>Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.

A:Reference number: A94309; MUID:76225080; PMID:9361108

A:Contents: annotation; disulfide bonds

R.Hoepflich, P.D.; Doolittle, R.F.

Biochemistry 22, 2049-2055, 1983

A>Title: Dimeric half-molecules of human fibrinogen are joined through disulfide bonds

A:Reference number: A90467; MUID:83231465; PMID:6860649

A:Contents: annotation; quaternary structure, disulfide bonds

R.Doolittle, R.F.

Annu. Rev. Biochem. 53, 195-229, 1984

A>Title: Fibrinogen and fibrin.

A:Reference number: A90041; MUID:64305751; PMID:6383134

A:Contents: annotation; review, EM structure, polymerization, ligands

R.Horwitz, B.H.; Varadi, A.; Scheraga, H.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 5980-5984, 1984

A>Title: Localization of a fibrin gamma-chain polymerization site within segment Thr-374

A:Reference number: A94006; MUID:85014892; PMID:6592597

A:Contents: annotation; polymerization region

R.Klotzsch, M.; Timmons, S.; Lukas, T.O.; Hawiger, J.

Biochemistry 23, 1767-1774, 1984

A>Title: Platelet receptor recognition site on human fibrinogen. Synthesis and structure

A:Reference number: A90483; MUID:84203545; PMID:636808

A:Contents: annotation; platelet aggregation region

R.Plow, E.F.; Strouj, A.H.; Meyer, D.; Marguerie, G.; Ginsberg, M.H.

J. Biol. Chem. 259, 5388-5391, 1984

A>Title: Evidence that three adhesive proteins interact with a common recognition site c

A:Reference number: A92477; MUID:84185664; PMID:6325435

A:Contents: annotation; platelet aggregation region

R.Dang, C.V.; Ebert, R.F.; Bell, W.R.

J. Biol. Chem. 260, 9713-9719, 1985

A>Title: Localization of a fibrinogen calcium binding site between gamma-subunit positic

A:Reference number: A92549; MUID:85261382; PMID:3160702

A:Contents: annotation; calcium binding region

R.Klotzsch, M.; Budzynski, A.Z.

J. Biol. Chem. 265, 13669-13676, 1990

A>Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH-te

A:Reference number: A37117; MUID:90337977; PMID:2143188

A:Contents: annotation, hementin cleavage site
 A>Note: Hementin, a protease from *Haemeteria ghiliani*, the giant South American leech,
 C:Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ization sites responsible for the formation of the soft clot.
 C:Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz-
 ing) and between alpha chains (weaker) of different monomers.
 C:Comment: All fibrinogen chains are synthesized in the liver.
 C:Comment: The two forms of gamma chain, A and B (see PIR:FGHUB), arise by alternate sp-
 licing, which makes this chain different from the gamma-B chain at positions 434-437 and
 C:Genetics:
 A:Gene: GDB:FCG
 A:Cross-references: GDB:119132; OMIM:134850
 A:Map position: 4q28-4q28
 A:Intons: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1; 433/3
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
 ins are contained in the core. Two three-chain coiled coils emerge from this core and co-
 from the distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
 F:126/Domain: signal sequence #status predicted <SIG>
 F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
 F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
 F:341-355/Domain: calcium binding #status predicted <CB>
 F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of an
 F:423-437/Region: platelet aggregation #status predicted
 F:54/Disulfide bonds: interchain (to gamma-35) #status experimental
 F:54/Disulfide bonds: interchain (to gamma-34) #status experimental
 F:49/Disulfide bonds: interchain (to beta-110) #status experimental
 F:49/Disulfide bonds: interchain (to alpha-64) #status experimental
 F:161/Disulfide bonds: carbhydrate (Asn) (covalent) #status experimental
 F:165/Disulfide bonds: interchain (to beta-227) #status experimental
 F:179-208/355-355/Disulfide bonds: interchain (to alpha-180) #status experimental
 F:424/Cross-link: isopeptide (Gln) (interchain to lys-422 N6-amino) #status experimental
 F:432/Cross-link: isopeptide (Lys) (interchain to Gln-424) #status experimental

Query Match 18.7%; Score 50.1; DB 1; Length 437;
 Best local similarity 29.4%; Pred. No. 3.6e-25;
 Matches 128; Conservative 57; Mismatches 140; Indels 110; Gaps 11;

QY 90 ELINNELKOKROIELTLOQVAVKVGIVSEVFLRK-----BSRNNSKRVOLY 138
 DB 53 DELSTVQTKVDDLOSLIEDILHVENKTSSEVKOLIKAIQLTVPDESSKPMIDATLKS 112
 QY 139 MOLLHEIIRKRNALSELQLENRIINOTADMQLASKYKDLKHKKYCHLATAHNSIILA 198
 DB 113 RKLLEETIK-----YEASILTDSIRYLOETINSNNQKTVN-----KEKVA 155
 QY 199 QLEHGOVPSARVPPOPPAPPRVYOPTFNRIINOISTELOSQDNMLKVLPPPLPTM 258
 DB 156 QLEAQOE-----PCK 166
 QY 255 PLTSLPSTDPKSGMRDCLQALDGHDTSSIVYKENTNRLMQWCCDRHDPGQTV 318
 DB 167 DTV-GIHDITGK-----DCODIANKAKQSGLYIKPKANQOFLVYCEIDSGNGTJV 219
 QY 319 IORRLDGSVNFERNMETYKQGFNID-----GEWYGLNENIYWLTFQO-----NYKLVTWEDW 372
 DB 220 FQKRLDGSVDFKKNMITYKEGFGHLSPTGTEFMIGNEKIHISTQSAIPALAVELEDF 279
 QY 373 SGRKFAEYASFRLEPSESYLYLGRY-HGNAGDS-----FTWNGKQFT 417
 DB 280 NERTSTADYAMKVPBEADKRLTLTAAYFAGDAGAFGPFQGDPSDKFSTSHNGQFS 339
 QY 418 TLDRDHVYTGCAHYQKGMWYNACASNLNNGWVYRGHVR-----SRYDDGYVMAEFR 472
 DB 340 TMDNDNDKFEKGCACQDQSGMMWMCCHAGHLNGLVYQGYTSKASTPNGYDNGILMAWK 399
 QY 473 GGSYSLEKVVMMIRP 487

DB 400 TRWYSKTKTWKIIIP 414

RESULT 8
 FGHUB
 fibrinogen gamma-B chain precursor [validated] - human
 N:Alternate names: coagulation factor I; fibrinogen gamma-55 chain.
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-1997 #sequence revision 17-Mar-1997 #text change 08-Dec-2000
 C:Accession: A90494; A92448; A90453; A28203; B28203; I37390; A03126
 R:Rixon, M.W.; Chung, D.W.; Davie, E.W.
 Biochemistry 24, 2077-2086, 1985
 A:Title: Nucleotide sequence of the gene for the gamma chain of human fibrinogen.
 A:Reference number: A90494; MUID:85252774; PMID:290550
 A:Accession: A90494
 A:Molecule type: DNA
 A:Residues: 1-113; 'I', 115-453 <RIX>
 A:Cross-references: GB:M10014; GB:J00134; GB:J00135; GB:X00086; NID:9182438; PION:AAB595
 J:Forname Jr., A.J.; Cummings, D.B.; Comeau, C.M.; Kant, J.A.; Crabtree, G.R.
 J Biol. Chem. 259, 12826-12830, 1984
 A:Title: Structure of the human gamma-fibrinogen gene. Alternate mRNA splicing near the
 A:Reference number: A92448; MUID:85030379; PMID:6092346
 A:Accession: A92448
 A:Molecule type: DNA
 A:Residues: 286-453 <FOR>
 R:Biochemistry 20, 6146-6149, 1981
 A:Title: Carboxy-terminal amino acid sequence of a human fibrinogen gamma-chain variant
 A:Reference number: A90453; MUID:82068993; PMID:7306501
 A:Accession: A90453
 A:Molecule type: Protein
 A:Residues: 411-434; 'Y', 436-440; 'Z', 442; 'Z', 444; 'B', 446-447; 'R', 449; 'ZBB', 453 <WOL>
 R:Francis, C.W.; Mueller, E.; Henschel, A.; Simpson, P.J.; Marder, V.J.
 Proc. Natl. Acad. Sci. U.S.A. 85, 3358-3362, 1988
 A:Title: Carboxyl-terminal amino acid sequences of two variant forms of the gamma-chain
 A:Reference number: A9194; MUID:88217900; PMID:3368448
 A:Accession: A28203
 A:Molecule type: Protein
 A:Residues: 433-449 <FRA>
 A:Accession: B28203
 A:Molecule type: protein
 A:Residues: 433-453 <FR2>
 R:Marchetti, U.; Zanelli, T.; Malcovati, M.; Tenchini, M.L.
 DNA Seq. 1, 419-422, 1991
 A:Title: Polymorphism of the human gamma chain fibrinogen gene.
 A:Reference number: I37390; MUID:92119334; PMID:1685103
 A:Accession: I37390
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 75-286 <RES>
 A:Cross-references: EMBL:X51473; NID:931410; PID:CA55837.1; PID:9930064
 C:Comment: The two forms of gamma chain, A (see PIR:FGHUB) and B, arise by alternate spl-
 licing, which makes this chain different from the gamma-B chain at positions 434-437 and
 C:Comment: The gamma-B chain is present in about 10% of the fibrinogen molecules in plas-
 C:Genetics:
 A:Gene: GDB:FCG
 A:Cross-references: GDB:119132; OMIM:134850
 A:Map position: 4q28-4q28
 A:Intons: 26/3; 41/3; 103/1; 134/2; 178/1; 222/3; 284/2; 377/1
 C:Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FG
 ins are contained in the core. Two three-chain coiled coils emerge from this core and co-
 from the distal domain nodes.
 C:Function:
 A:Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A:Pathway: blood coagulation
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C:Keywords: alternative splicing; blood coagulation; calcium; coiled coil; glycoprotein;
 F:126/Domain: signal sequence #status predicted <SIG>
 F:27-437/Product: fibrinogen gamma-A chain #status experimental <MPT>
 F:176-415/Domain: fibrinogen beta/gamma homology <FBG>
 F:341-355/Domain: calcium binding #status predicted <CB>
 F:400-422/Region: polymerization site, binding to the amino end of the alpha chain of an
 F:423-437/Region: platelet aggregation #status predicted

F;75-324/Domain: fibrinogen beta/gamma homology <FBG>

D5 163 LNNILGNHYAKYKFKRGDSFSELDVVGAIISGIAGDSDWIKINNTNCTIENEDNCVQ

Db 163 LNNTLGNYAKYKFRIGDSFSEYLLVLGAYSSGLAGDSL

163 T N N T T G N H Y Y A K Y N K F R T G D S F S E Y L L V I G A Y S G T A G D S L A Y H N T M R F S T Y D N D N D V Y S I 222

Db 163 LNNTLGNHYAKYNKFRIGDSFSEYLLVLGAYSGTAGDSLAYHNTMRFSTYDNDNDVYSI 222

QY 429 NCA--HYOKGWMYNAACHSNNINGVWYRGHYRSHYODGVYWAFFRGSGYSILKVVMMI 485
 DB 223 NCASHSSYSGAWMYXSCILSNLNGQY---DYSG--APSIWYSYLPBNDQIPFAEMKL 277
 QY 486 R 486
 DB 278 R 278

RESULT 11

A32670
 fibrinogen gamma chain - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 13-Aug-1999
 C:Accession: A32670; 151416
 R:Pastori, R.L.; Moskaitis, J.E.; Smith Jr., L.H.; Schoenberg, D.R.
 Biochemistry 29, 2599-2605, 1990
 A>Title: Estrogen regulation of Xenopus laevis gamma-fibrinogen gene expression.
 A:Reference number: A32670; PMID:90241882; PMID:2334684
 A:Accession: A32670
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-438 <PAS>
 A:Cross-references: GB:J02894; NID:G214139; PIDN:AAA49709.1; PID:G214140
 R:Bhattacharya, A.; Shepard, A.R.; Moser, D.R.; Holland, L.J.
 Mol. Cell. Endocrinol 72, 213-220, 1990
 A>Title: Isolation and characterization of cDNA clones for the gamma subunit of Xenopus
 A:Reference number: 151416; PMID:91146806; PMID:2289632
 A:Accession: 151416
 A>Status: Preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-58 <BHA>
 A:Cross-references: GB:M35548; NID:G214141; PIDN:AAA03247.1; PID:G214142
 C:Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 C:Keywords: blood coagulation
 F:173-413/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.2%; Score 489.5; DB 2; Length 438;
 Best Local Similarity 31.4%; Pred. No. 2e-24;
 Matches 125; Conservative 54; Mismatches 154; Indels 65; Gaps 13;
 QY 145 IIRKDNALLESQENRILNQTADMLQASKKY---DLEHKYQHLATLAHQSEI1A9 199
 DB 25 IIPNTDNCILDRGEYCEPTTCGISDFLNRYQENVDTLQY-DENLLTQISNSTGTTI 83
 QY 200 LEEHQGVPSA-RPVQPPAPAPRVYQPT-----YKRIINQISTNFIQSDN 247
 DB 84 IVEHL--IDSGKKPATSFQTAIDPVTQKSTCKMKTMDKMYVQYEENILYLQEVSSNQ 141
 QY 248 LKV-----LPPPLPTMPTLTSPPSSTDKSPGWRDCLQALDGHDTSSIYLKP 296
 DB 142 NKIFLLQKIANLELQCCQCPGRDVT-QIQEFTGK-----DQGVANKGAMLSGLYIKP 194
 QY 297 ENTNRILMQVWDQRRHDPGWTVIQRLDGSVNFRRNMTYKQSGF---NIDGEYWLGLE 352
 DB 195 LKAKQCFIVCEIEBSSGAWTVIORLDGSVNFHKNWQYEGEGYLSPPDKTEFFWVGN 254
 QY 353 NIYMLTNGN--YKLLVTMEDSGRKVAEYASFLPESESEYKLRGRY-HGNAGDSF- 408
 DB 255 KIHLLSTGSLPIYWRILEDMNSQKSTADYSTRLSGKKNYFTYAFYIGDAGAFD 314
 QY 409 -----TWANGKOTTLDRDHVYTGCAHYQKGGWYNAACHSNNINGVWYRG 455
 DB 315 GFDGDDPSDKFYTSNMQPSTFDKNDKEDGCAODSGGMMNRCFAAHLNGKYYQG 374
 QY 456 GHYR-----SRYODGVYWAFFRGSGYSILKVVMMIRP 487
 DB 375 GTYSEADSGPSGYNGLINATWRKRYMSKSVTKMIP 412

RESULT 12
 A45445
 Janusin precursor, long form - rat

N:Alternate names: neural recognition glycoprotein J1-160/180, long form
 N:Contents: neural recognition glycoprotein J1-160/180, short form
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 20-Aug-1999
 C:Accession: A45445; B45445; S32023
 R:Fuss, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.
 J. Cell Biol. 120, 1237-1249, 1993
 A>Title: Molecular characterization and in situ mRNA localization of the neural recognit
 A:Reference number: A45445; PMID:9311267; PMID:769676
 A:Accession: A45445
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1356 <FUS>
 A:Cross-references: GB:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962
 A:Accession: B45445
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-772,863-1356 <FUD>
 A:Cross-references: GB:Z18630
 R:Fuss, B.; Wintergerst, E.; Bartsch, U.; Schachner, M.
 submitted to the EMBL Data Library, November 1992
 A>Description: Molecular characterization and in situ mRNA localization of the neural re

A:Reference number: S32023
 A:Accession: S32023
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1356 <FUS2>
 A:Cross-references: EMBL:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962
 C:Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
 C:Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; oligo
 F:1-1356/Product: janusin, long form #status experimental <XAT>
 F:1-772,863-1356/Product: janusin, short form #status experimental <ALT>
 F:204-230/Domain: EGF homology <EG1>
 F:235-261/Domain: EGF homology <EG2>
 F:266-292/Domain: EGF homology <EG3>
 F:297-323/Domain: EGF homology <EG4>
 F:325-405/Domain: fibronectin type III repeat homology <FN1>
 F:413-494/Domain: fibronectin type III repeat homology <FN2>
 F:502-584/Domain: fibronectin type III repeat homology <FN3>
 F:582-576/Domain: fibronectin type III repeat homology <FN4>
 F:684-764/Domain: fibronectin type III repeat homology <FN5>
 F:772-854/Domain: fibronectin type III repeat homology <FN6>
 F:1038-1118/Domain: fibronectin type III repeat homology <FN7>
 F:1133-1341/Domain: fibronectin beta/gamma homology <FBG>

Query Match 18.2%; Score 488; DB 2; Length 1356;
 Best Local Similarity 36.2%; Pred. No. 1.2e-23;
 Matches 109; Conservative 41; Mismatches 103; Indels 48; Gaps 7;
 QY 215 QPPAPAPRVYQPPYTRIRIINQISTNFIQSDNKLKVLPPPLPTMPTLNSPESDXP--- 271
 DB 1060 QPPRAA-----IENVLYTKSTDSGRKELIVDAEDTWRLEGLSENIDYTVLL 1107
 QY 272 -----SGPWRDCLQALDGHDTSSIYL--KPENTNRILMQV 306
 DB 1108 QAAQEAATRSLSLTSTFTTGGRVFSHP-QDCAQHLNNGDTLSGVYTIPLNGELSHKL-QVY 1165
 QY 307 CQGRHDPGWTVIQRLDGSVNFRRNMTYKQSGFNTIGEWLGLENTYMLTNGNTYLL 366
 DB 1166 CMTTDDGGWIVFQRQNGQDTPFRKMWADYRGFNLEDEPMLGJDNHRTTAQGRYELR 1225
 QY 367 VTMEDSGRKVAEYASFLPESESEYKLRGRYHGNAGDSFTWANGKQFTLLDRDHVY 426
 DB 1226 VDMRD-QGEAVYAYDKFAVEDSRSLYKLRIGVYGTAGDLSHYQGRFFSTEDBDNVA 1284
 QY 427 TQNCAYQKGGWYNAACHSNNINGVWYRGHYRSHYODGVYWAFFRGSGYSILKVVMMIR 486
 DB 1285 VTNCAMSYKGAWMYXNCHRTYLN-----GKYGESHSQGIWYHWKGFESIPVEMQCR 1339
 QY 487 P 487
 DB 1340 P 1340

RESULT 13

B47172
 ficollin-beta - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C/Accession: B47172
 R/Title: H. Hellman, U. Weststedt, C. Gopez, L.J., Claesson-Welsh, L., Heidén, C.H., J. Biol. Chem. 268, 14505-14513, 1993
 U/Title: Molecular cloning and characterization of ficollin, a multimeric protein with 74
 A/Reference number: A47172; UID:93300852; PMID:7686157
 A/Accession: B47172
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-326 <ICH>
 A/Cross-references: GB:U12345; NID:9294219; PIDN:AAC69641.1; PID:91228925
 A/Experimental source: uterus
 A/Note: sequence extracted from NCBI backbone (NCBI:134468, NCBI:P:134470)
 C/Superfamily: fibrinogen beta/gamma homology
 F:115-326/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.0%; Score 484.5; DB 2; Length 326;
 Best Local Similarity 46.6%; Pred. No. 2.8e-24;

Matches 103; Conservative 35; Mismatches 68; Indels 15; Gaps 6;

QY 272 SGPWRDCLQALDEGDHDS---SIYL-VKPEENTRLMOVWCDQRHDPGGMVYIQRRLDGS 326
 DB 113 TGP-RCKKELLTRGHFLSGMHTIYLPDCP-----LTVLCMDMDTDGGGMVYFQRMDGS 165
 QY 327 VNFERNETKQGFQNDIEYMLGLENTYMLTNOGNKYLVTMEDMSGRKYFAEYASRL 386
 DB 166 VDFYDMAVYKQGFQSGQGEFWMGNDHIALTAQSSSLRDLVDVFEHNGPAKTKSRVQV 225
 QY 387 ESEYKRLRGY-HGNAGDSFTWANGKQFTTLDRHDVYTGNCAYKQKGMWYACAHN 445
 DB 226 AGEAEKYLVLGAFVQSGAGNSLTGHNHNFSTKQDNDVSSNCAEKFQGMWYADCHASS 285
 QY 446 SNLNGVWYRGHYSRYQDGVYMAEPRGSGYSLKVVMMIR 486
 DB 286 SNLNGRYLRGLH--TSYANGVWVRSGRGYVSYQVSEKVR 324

RESULT 14

S61517
 ficollin-1 precursor - human
 N/Alternate names: 36K HLA-cross-reactive plasma protein, hucollin, 35K
 C/Species: Homo sapiens (man)
 C/Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 18-Feb-2000
 C/Accession: S61517; J04942
 R/Title: U. J. Tay, P.N.; Kon, O.L.; Reid, K.B.M.
 Biochem. J. 313, 473-478, 1996
 A/Title: Human ficollin: cDNA cloning, demonstration of peripheral blood leucocytes as th
 A/Reference number: S61517; UID:96152529; PMID:8573080
 A/Accession: S61517
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-326 <LU>
 A/Cross-references: GB:S60990; NID:91911529; PIDN:AAB50706.1; PID:91911530
 R/Hartmulya, S.; Takeda, K.; Sugitani, T.; Fukumoto, Y.; Tachikawa, H.; Miyazono, K.; Fujii
 J. Biochem. 120, 745-751, 1996
 U/Title: Characterization of ficollins as novel elastin-binding proteins and molecular cl
 A/Reference number: J04942; UID:97103465; PMID:8947836
 A/Accession: J04942
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 8-132; 'T', 134-286, 'N', 288-326 <HAR>
 A/Cross-references: DDBJ:D83920; NID:91510126; PIDN:BA12120.1; PID:915101
 C/Experimental source: uterus
 C/Comment: This is an elastin-binding plasma protein.
 C/Superfamily: fibrinogen beta/gamma homology
 C/Keywords: glycoprotein, plasma
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:52-108/Region: collagen-like

F:115-326/Domain: fibrinogen beta/gamma homology <FBG>
 F:305/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.0%; Score 483.5; DB 2; Length 326;
 Best Local Similarity 45.9%; Pred. No. 3.3e-24;

Matches 101; Conservative 39; Mismatches 69; Indels 11; Gaps 6;

QY 272 SGPWRDCLQALDEGDHDS---SIYLVPENTNRLMOVWCDQRHDPGGMVYIQRRLDGSV 328
 DB 113 TGP-RNCKDLIDRGYFLSGMHTIYLPDCP-----LTVLCMDMDTDGGGMVYFQRMDGSVD 167
 QY 329 VNFERNETKQGFQNDIEYMLGLENTYMLTNOGNKYLVTMEDMSGRKYFAEYASRLAE 388
 DB 168 VDFYDMAVYKQGFQSGQGEFWMGNDHIALTAQSSSLRDLVDVFEHNGPAKTKSRVAD 227
 QY 389 ESEYKRLRGY-HGNAGDSFTWANGKQFTTLDRHDVYTGNCAYKQKGMWYACAHN 447
 DB 228 EAEKYKLVLAGFVQSGAGNSLTGHNHNFSTKQDNDVSSNCAEKFQGMWYADCHASS 287
 QY 448 LNGVWYRGHYSRYQDGVYMAEPRGSGYSLKVVMMIR 487
 DB 288 LNLGLYLMGPH--ESYANGVWVRSGRGYVSYQVSEKVR 325

RESULT 15

A27447
 cytotoxic T-lymphocyte-specific protein precursor (clone pT49) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 03-Dec-1999
 C/Accession: A27447
 R/Koyama, T.; Hall, L.R.; Hasegawa, W.G.; Tonegawa, S.; Saito, H.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1609-1613, 1987
 A/Title: Structure of a cytotoxic T-lymphocyte-specific gene shows a strong homology to
 A/Reference number: A27447; UID:87175527; PMID:3550794
 A/Accession: A27447
 A/Molecule type: mRNA
 A/Residues: 1-432 <KRY>
 A/Cross-references: GB:M16238; NID:9193304; PIDN:AAA7624.1; PID:9387156
 C/Superfamily: fibrinogen gamma chain; fibrinogen beta/gamma homology
 F:203-428/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 18.0%; Score 483.5; DB 2; Length 432;
 Best Local Similarity 26.3%; Pred. No. 4.8e-24;

Matches 136; Conservative 84; Mismatches 164; Indels 133; Gaps 17;

QY 9 W-WL-GILAMGAVAGDEGFEGTEGSPREFTYLRKYRAGEGQ-DKCTYFIVPQOR 64
 DB 6 WMLSSAVLACRAVE-EHNTBLEDSAQACPA-RLESGRGESGQCFQTLPLT 63
 QY 65 VTGAICVNSKEPEVLENNVHKQELINELLKQKQIE-----T 105
 DB 64 IQLPRQGSME-EVLKEVRLTKEAVDSLKSCQDCQLQADHRDPGNGNGAETABDSR 122
 QY 106 LQQLKVDGIVSEYKYLKRESRMNNSVYQLWQLLHEIRKQDNMLELSQLNRILNQ 165
 DB 123 VQLESQVNRKLSSELKAKKQDQIGQGLTFLHL-----VNANNIENYDNR 169
 QY 166 TADMQLASKYKDEHKYQHLATLAHQSEIIIAOLEHQCQVPSPAPVPPAPPRVY 225
 DB 170 VA-----NLTVVNSIDGCKSPGEHQSOV----- 198
 QY 226 QPPTNRIINQISTNEISDQNLKLPPLPLTMTPLTSLPSTDPKSPPMWDCQALBDG 285
 DB 199 -----QHL-----TYDCSDHYLG 213
 QY 266 HDTSTIYLKPEENTNRLMOVWCDQRHDPGGMVYIQRRLDGSVNFERNETKQGFQND 345
 DB 214 RSGSAYAVTPPHRNSFEVYCDMETGGMVYCARLDGSTNFTREWKYKAGFQNDLR 273
 QY 346 EYWLGLENIYMLTNOGNKYLVTMEDMSGRKYFAEYASRLAESEYKRLRGYHNG 405
 DB 274 EFWLGNDXIHLLTKSEKEMILRIDEDFNGLTLYALYQDFYANEFLLKRYLHIGNYTAG 333

QY 406 DSFTW-----HNGKQFTTLD RDHDVY-TGNC AHYKGGWVWYNACAHSNLNGVWYRGHYR 459
Db 334 DALRFSRHVNHDLRFPTTDPDNDRYPSGNCGLYSSGWFDSCLSANLNGKY--HOK 390
QY 460 SR-YQDGVYWAFFRG-----GSY--SLKXVMMIRP 487
Db 391 YKGVNNGIFWGTWPGINQAPGCGYKSSFKQAKMMIRP 427

Search completed: July 30, 2004, 12:38:01
Job time : 19 secs

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OK protein - protein search, using sw model

Run on: July 30, 2004, 12:19:33 ; Search time 13 Seconds
(without alignments)
1974.660 Million cell updates/sec

Title: US-10-018-386-2

Perfect score: 2666
Sequence: 1 MRPLCTCTGWLGLIANGAV.....GSYSLKRYVMIRNPPTPH 493

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score-distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2682	99.9	493	1 ANL2_HUMAN	Q9ak99 homo sapien
2	2550	94.9	493	1 ANL2_MOUSE	Q97045 mus musculu
3	577	21.5	497	1 AGP1_RAT	O35460 rattus norv
4	575.5	21.4	498	1 AGP1_MOUSE	O08538 mus musculu
5	574	21.4	496	1 AGP2_HUMAN	O15123 homo sapien
6	572.5	21.3	498	1 AGP1_HUMAN	O15389 homo sapien
7	558	20.8	509	1 AGP4_MOUSE	O95765 mus musculu
8	541	20.1	503	1 AGP4_HUMAN	O09264 homo sapien
9	537	20.0	312	1 FGL1_HUMAN	O08830 homo sapien
10	537	20.0	496	1 AGP2_PIG	O18920 bos taurus
11	536.5	19.9	481	1 AGP1_BOVIN	O35608 mus musculu
12	535.5	19.9	496	1 AGP2_MOUSE	O02675 homo sapien
13	527.5	19.6	468	1 FIBB_BOVIN	P02676 bos taurus
14	526.5	19.6	491	1 FIBB_HUMAN	P02675 homo sapien
15	524	19.5	741	1 FIBB_CHICK	P14448 gallus gall
16	522.5	19.5	479	1 FIBB_RAT	P14480 rattus norv
17	520.5	19.4	866	1 FIBB_HUMAN	P02671 homo sapien
18	512.5	19.1	477	1 FIBB_PETMA	P02678 petromyzon
19	506.5	18.9	299	1 FIBB_HUMAN	O75636 homo sapien
20	505	18.8	782	1 FIBB_RAT	P06399 rattus norv
21	504.5	18.8	375	1 AGP2_BOVIN	O70497 mus musculu
22	503.5	18.7	306	1 FCN2_MOUSE	O13485 homo sapien
23	503.5	18.7	313	1 FCN2_HUMAN	Q02020 gallus gall
24	503	18.7	463	1 FIBB_CHICK	Q02020 gallus gall
25	501	18.7	453	1 FIBB_HUMAN	P19477 parastichop
26	495	18.4	282	1 FIBB_PARPA	P17654 xenopus lae
27	489.5	18.2	438	1 FCN1_HUMAN	O00602 homo sapien
28	488.5	18.2	326	1 FCN1_HUMAN	P55083 homo sapien
29	486.5	18.1	255	1 MPA4_HUMAN	P12804 mus musculu
30	483.5	18.0	432	1 FGL2_MOUSE	O70465 mus musculu
31	482.5	18.0	334	1 FCN1_MOUSE	O14314 homo sapien
32	480.5	17.9	439	1 FGL2_HUMAN	P57756 rattus norv
33	479.5	17.9	319	1 FCN2_RAT	

34	476.5	17.7	444	1 FIBB_BOVIN	P12799 bos taurus
35	473	17.6	335	1 FCN1_RAT	O9wrs8 rattus norv
36	471	17.5	445	1 FIBB_RAT	P02680 rattus norv
37	465.5	17.3	641	1 FIBB_PETMA	P33573 petromyzon
38	463.5	17.3	432	1 FIBB_CHICK	O4115 petromyzon
39	450.5	16.8	1808	1 TENA_CHICK	P10039 gallus gall
40	450	16.8	4289	1 TENX_HUMAN	P22105 homo sapien
41	434.5	16.2	1746	1 TENA_PIG	O29116 sus scrofa
42	430.5	16.0	1294	1 TENN_HUMAN	O9udp3 homo sapien
43	424.5	15.8	1560	1 TENN_MOUSE	O80271 mus musculu
44	423	15.7	406	1 ANL4_HUMAN	Q9b766 homo sapien
45	421.5	15.7	2201	1 TENA_HUMAN	P24821 homo sapien

ALIGNMENTS

RESULT 1
ANL2_HUMAN STANDARD; PRT; 493 AA.
ID ANL2_HUMAN
AC Q9ak99;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiotensin-related protein 2 precursor (Angiotensin-like 2)
DE (UNQ170/PRO196).
GN ANGPRT2 OR ARP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G.,
RA Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiotensin-
RT related protein. angiotensin-related protein induces endothelial cell
RT sprouting.";
RL J. Biol. Chem. 274:26523-26528(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Denel B., Dowd P.,
RA Bacon D., Foster J., Grimaldi C., Gu O., Hass P.E., Helens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Sestagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yamsura D.,
RA Yi S., Yu G., Yuan J., Zhang W., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=ovary;
RX MEDLINE=22386257; PubMed=12477932;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diachenko L., Marushina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Roach S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Wadon A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., R. Scheraga A., Schein J.E., Jones S.J.M., Maira W.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: Induces sprouting in endothelial cells through an autocrine and paracrine action.

- SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECIFICITY: Widely expressed in heart, small intestine, spleen and stomach. Also found in lower levels in colon, ovary, adrenal gland, skeletal muscle and in prostate.

- PTM: N-glycosylated.

- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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EMBL: AF125175; AAD55357.1; -
EMBL: AF358274; AAO8641.1; -
EMBL: BC013368; AAI12368.1; -
HSSP: P02671; 1FZD.
GeneW: HGNC:490; ANGPTL2.
MIM: 605001; -
GO: GO:0005615; Cytoplasmic space; TAS.
GO: GO:0005102; F:receptor binding; TAS.
GO: GO:0007275; P:development; TAS.
InterPro: IPR002181; Fibrinogen_C.
Pfam: PF00147; fibrinogen_C_1.
SMART: SM00186; FBG; 1.
PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
KW signal; coiled coil; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 493 ANGIOPOIETIN-RELATED PROTEIN 2.
FT DOMAIN 76 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 206 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT DISULFID 278 307 BY SIMILARITY.
FT DISULFID 430 443 BY SIMILARITY.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 493 AA; 57104 MW; 0F2ADCEB53D185CA CRC64;

Query Match 99.9%; Score 2682; DB 1; Length 493;
Best Local Similarity 99.8%; Pred. No. 1-3e-159;
Matches 492; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 MRPLCVTGMWGLLAAMGAVAGQEDGFEETGSGPREFTYINRYKRAESGDKCTYFTIV 60
1 MRPLCVTGMWGLLAAMGAVAGQEDGFEETGSGPREFTYINRYKRAESGDKCTYFTIV 60
61 POORVTGAICVNSKEPEVLLENRYKKELELNELLKOKOITLQOYVNGDGYSEV 120
61 POORVTGAICVNSKEPEVLLENRYKKELELNELLKOKOITLQOYVNGDGYSEV 120
121 KLRRKESNNNSRVYQYVQMLHEIRKEDNALSOLENNILNQTDMLQASKYDLE 180
121 KLRRKESNNNSRVYQYVQMLHEIRKEDNALSOLENNILNQTDMLQASKYDLE 180
121 KLRRKESNNNSRVYQYVQMLHEIRKEDNALSOLENNILNQTDMLQASKYDLE 180
181 HKYGLATLANNOSEITIAOLEHQCQVPSAPVQPPAPAPRYQPTNRIINQSTN 240
181 HKYGLATLANNOSEITIAOLEHQCQVPSAPVQPPAPAPRYQPTNRIINQSTN 240
241 EIQSDONIKVLPPLPTWPTLTSPSSSTDKSGGWRDCLQALSDGHTSSIVYKPENTN 300
241 EIQSDONIKVLPPLPTWPTLTSPSSSTDKSGGWRDCLQALSDGHTSSIVYKPENTN 300

301 RIMQWGDQHRDPCGWTVIQRLDGSVNFRRMNETYKQSGCNIDGFWLGLENIYMLTNQ 360
301 RIMQWGDQHRDPCGWTVIQRLDGSVNFRRMNETYKQSGCNIDGFWLGLENIYMLTNQ 360
361 GNYVLATVMEQSGRKYFAEYASFRLEPSEYKLRGRHGNACDSFTWHNKGFTLLD 420
361 GNYVLATVMEQSGRKYFAEYASFRLEPSEYKLRGRHGNACDSFTWHNKGFTLLD 420
421 RDHVVYTGNCAPHYKQSGWYNACASHNLNGVYRGGHYRSRYDDGYWAEFRGGSYLKK 480
421 RDHVVYTGNCAPHYKQSGWYNACASHNLNGVYRGGHYRSRYDDGYWAEFRGGSYLKK 480
481 VVMMIRPNPTFH 493
481 VVMMIRPNPTFH 493
481 VVMMIRPNPTFH 493

RESULT 2
ANL2_MOUSE STANDARD; PRT; 493 AA.
ID ANL2_MOUSE
AC Q9R045;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-related protein 2 precursor (Angiopoietin-like 2).
GN ANGPTL2 OR ARP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99403103; PubMed=10473614;
RA Kim I., Moon S.-O., Koh K.N., Kim H., Uhm C.-S., Kwak H.J., Kim N.-G., Koh G.Y.;
RT "Molecular cloning, expression, and characterization of angiopoietin-related protein, angiopoietin-related protein induces endothelial cell sprouting."
RT J. Biol. Chem. 274:26523-26528(1999).
CC - FUNCTION: Induces sprouting in endothelial cells through an autocrine and paracrine action (By similarity).
CC - SUBCELLULAR LOCATION: Secreted (By similarity).
CC - TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEART, TONGUE, LUNG AND SKELETAL MUSCLE. ALSO FOUND IN LOWER LEVELS IN KIDNEY, EPIDIDYMUS AND TESTIS.
CC - SIMILARITY: Contains 1 fibrinogen C-terminal domain.

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EMBL: AF125176; AAD55358.1; -
HSSP: P02671; 1FZD.
WGI: WGI:1347002; Angptl2.
InterPro: IPR002181; Fibrinogen_C.
Pfam: PF00147; fibrinogen_C_1.
SMART: SM00186; FBG; 1.
PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
KW signal; coiled coil; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 493 ANGIOPOIETIN-RELATED PROTEIN 2.
FT DOMAIN 77 115 COILED COIL (POTENTIAL).
FT DOMAIN 152 202 COILED COIL (POTENTIAL).
FT DOMAIN 438 450 FIBRINOGEN C-TERMINAL.
FT DISULFID 278 307 BY SIMILARITY.
FT DISULFID 430 443 BY SIMILARITY.
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 192 192 N-LINKED (GLCNAC...) (POTENTIAL)
 SQ SEQUENCE 493 AA; 57118 MW; 228855ABEF0746BF2 CRC64;
 Query Match 94.9%; Score 2550; DB 1; Length 493;
 Best Local Similarity 94.7%; Pred. No. 2,1e-151;
 Matches 467; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 1 MRPLCTCWMIGLAAAGAVAGQEDGFGTEEGSFRRTIYINRYRAGESQDKTYFTIV 60
 DB 1 MRPLCTCWMIGLAAAGAVAGQEDGFGTEEGSFRRTIYINRYRAGESQDKTYFTIV 60
 QY 61 PQRATGAI CVNSKEPEVLENRVAKOELINNELKOKQOIEITLOQVAVDGIASEV 120
 DB 61 PQRATGAI CVNSKEPEVLENRVAKOELINNELKOKQOIEITLOQVAVDGIASEV 120
 QY 121 KLRKESRNNRSRYTQVYVQLHEIRKRDNALELSQENRIINQADMLQASKYKDL 180
 DB 121 KLRKESRNNRSRYTQVYVQLHEIRKRDNALELSQENRIINQADMLQASKYKDL 180
 QY 181 HKYGLATLANOSSEITIAOLEHCORVPSARVPVPPAPAPRYVQPTNRIINQSTN 240
 DB 181 HKYGLATLANOSSEITIAOLEHCORVPSARVPVPPAPAPRYVQPTNRIINQSTN 240
 QY 241 EIOSQONIKVLPPLPTMPTLTSLPSSTDKPSGPRDCLQALEDHSTSIYLVKPENTN 300
 DB 241 EIOSQONIKVLPPLPTMPTLTSLPSSTDKPSGPRDCLQALEDHSTSIYLVKPENTN 300
 QY 301 RIMQVWCDQDHPGQATVIQRRLDGSVNFERNWETKQFGNIDCEYVGLNFIYMLNQ 360
 DB 301 RIMQVWCDQDHPGQATVIQRRLDGSVNFERNWETKQFGNIDCEYVGLNFIYMLNQ 360
 QY 361 GNYKLVLMEDMSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTILD 420
 DB 361 GNYKLVLMEDMSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTILD 420
 QY 421 RDHDVYTGCAHYQKQGMWYNA CAHSNINLVNVRGGRYRSRYQDGVYAAEFRRGSSYSIKK 480
 DB 421 RDHDVYTGCAHYQKQGMWYNA CAHSNINLVNVRGGRYRSRYQDGVYAAEFRRGSSYSIKK 480
 QY 481 VVMATIRPENTFH 493
 DB 481 VVMATIRPENTFH 493

RESULT 3
 ACPI RAT STANDARD; PRT; 497 AA.
 ID ACPI RAT STANDARD; PRT; 497 AA.
 AC 035460; Q8K4Q4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensin-1 precursor (ANG-1).
 GN ANGPL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Histar; TISSUE=Placenta;
 RX MEDLINE=2236496; PubMed=12458664;
 RA Tizasa H., Bae S.H., Asashima T., Kitan T., Matsunaga N.,
 RA Teraaki T., Kang Y.S., Nakashima E.,
 RT "Augmented expression of the tight junction protein occludin in brain
 RT endothelial cell line TR-bBB by rat angiotensin-1 expressed in
 RT baculovirus-infected sf plus insect cells.";
 RL Pharm. Res. 19:1757-1760(2002).
 RN [2]
 RP SEQUENCE OF 91-200 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Placenta;
 RX MEDLINE=98451564; PubMed=976732;
 RA Mandiote S.J., Pepper M.S.,
 RT "Regulation of angiotensin-2 mRNA levels in bovine microvascular

RT endothelial cells by cytokines and hypoxia".
 RL Circ. Res. 83:852-859(1998).
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL; AB080023; BAC10290.1; -
 CC InterPro; IPR002181; Fibrinogen_C.
 CC Pfam; PF00147; Fibrinogen_C; 1.
 CC SMART; SM00514; FIBRIN AG C DOMAIN; 1.
 CC PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 CC KEGG; Angiogenesis; Glycoprotein; Coiled coil; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 497
 CC DOMAIN 81 119
 CC DOMAIN 153 261
 CC DOMAIN 283 497
 CC DISULFID 285 314
 CC DISULFID 438 451
 CC CARBOHYD 92 92
 CC CARBOHYD 122 122
 CC CARBOHYD 154 154
 CC CARBOHYD 243 243
 CC CARBOHYD 294 294
 CC CONFLICT 98 98
 CC CONFLICT 172 172
 CC CONFLICT 189 189
 CC SEQUENCE 497 AA; 57461 MW; 08E6A8B8FDB68AF CRC64;
 Query Match 21.5%; Score 577; DB 1; Length 497;
 Best Local Similarity 29.5%; Pred. No. 8.7e-29;
 Matches 149; Conservative 84; Mismatches 170; Indels 102; Gaps 14;

QY 43 RYKRGESQDKCTYFTIV-----QQRVTAICVNSKEPEV-----L 79
 DB 32 RYNIQHQG--CATFTLPEHDGCRGASATQVYTNALQDAPAVETDFSSQKQHLH 89
 QY 80 LENRVHKOELINNELK-OKRQIEITLQ-----LVKQDGIASEVKKLRKESRN 129
 DB 90 MEN--YQWQKQLENIYVENKSEMAQIQQAVQNTATMLEIGTSLSC---AEQTRK 144
 QY 130 MNSRYTQVYVQLHEIRKRDNALELSQENRIINQADMLQASKYKDLHKY----- 183
 DB 145 LTVETQVYVQLHEIRKRDNALELSQENRIINQADMLQASKYKDLHKY----- 204
 QY 184 -----CHLATLANOSSEITIAOLEHCORVPSARVPVPPAPAPRYVQPTN 231
 DB 205 HKEELDTLKEKENLQGLVTRQRTILGELBQSLRA----- 240
 QY 232 RIINQISNIEIQSQONIKVLPPLPTMPTLTSLPSSTDKPSG-----PQRDCLQAL 284
 DB 241 -----TSNNSVLQKQOEL-----MDYVNIIVSLCTKVKLLKGRREERPRDCAVYQA 291
 QY 285 GHDTSSIVLVKPENTNRLMQVWCDQDHPGQATVIQRRLDGSVNFERNWETKQFGNID 344
 DB 292 GPNNSGIITTYFNNMPEPKYFCAMDVNEGWTYIQHREDSDLDFQGWKEXKMGFGNPS 351
 QY 345 GEYVGLNFIYMLNQGYKLVLMEDMSGRKVFAYASFRLEPSEYKRLGRYHGN 404

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Db 352 GGYWLNDEFIATSRQWYLRLEIMDEGNRAVSQYDFH:GNQKQRYLTLKCHTGA 411
Qy 405 G--DSTWNGKQFTLLDHDVYTGNCNCHYKGGWYTAACHSNLNGWYFGGHRSR 462
Db 412 GQSSSLIHL-GADFSFKDADNDNCMKCALMLTGWMPDAGSPSLNMGFYTAGQNHGL 470
Qy 463 ODGYWAEPFGSGSLKXVMMIRP 487
Db 471 -NGIKWHYFKGSPYSLSRTTMMIRP 494

RESULT 4
AGP1_MOUSE STANDARD; PRT; 498 AA.
ID AGP1_MOUSE
AC 008538;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-1 precursor (ANG-1).
GN ANGPT1 OR AGPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=97334663; PubMed=8980223;
RA Davis S., Aldrich T.H., Jones P.F., Acheson A., Compton D.L., Jain V.,
RA Ryan T.E., Bruno J., Radziejewski C., Malsompiere P.C.,
RA Yancopoulos G.D.;
RT "Isolation of angiopoietin-1, a ligand for the Tie2 receptor, by
RT secretion-trap expression cloning."
RL Cell 87(1):1161-1169(1996).
CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
CC HEART EARLY DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: EARLY IN DEVELOPMENT, AT E9 TO E11, IT IS
CC FOUND MOST PROMINENTLY IN THE HEART MYOCARDIUM SURROUNDING THE
CC ENDOCARDIUM. LATER, IT BECOMES MORE WIDELY DISTRIBUTED, MOST OFTEN
CC IN THE MESENCHYME SURROUNDING DEVELOPING VESSELS, IN CLOSE
CC ASSOCIATION WITH ENDOTHELIAL CELLS.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U83509; A835058.1; -.
CC HSSP: P02671; 1F2D.
CC MCD: MGI:108448; Agpt.
CC GO: GO:0007163; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
CC InterPro: IPR002181; Fibrinogen_C.
CC Pfam: PF00147; fibrinogen_C; 1.
CC SMART: SMC0186; FBG; 1.
CC PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
CC Angiogenesis; Glycoprotein; Coiled coil; Signal.
CC SIGNAL
CC CHAIN 1 19
CC POTENTIAL.
CC ANGIOPOIETIN-1.
CC DOMAIN 81 119
CC COILED COIL (POTENTIAL).
CC DOMAIN 153 261
CC COILED COIL (POTENTIAL).
CC DOMAIN 284 498
CC FIBRINOGEN C-TERMINAL.
CC DISULFID 286 315
CC BY SIMILARITY.
CC FT DISULFID 439 452
CC BY SIMILARITY.

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FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 498 AA; 57505 MW; 285B4FDEC26D800 CRC64;

Query Match 21.4%; Score 575.5; DB 1; Length 498;
Best Local Similarity 29.8%; Pred. No. 1,1e-28;
Matches 151; Conservative 83; Mismatches 169; Indels 103; Gaps 15;

Qy 43 RYKRGESQDKCTYTFIVP-----QQRVGAICVSKR-EP-----EVL 79
Db 32 RYMRICQGO--CAVTFILPEHDCNCRSAEYQYNTNALQRDAPHYEPDESSQYLGHEHY 89
Qy 80 LERNVHKQELINLNLTK-QKROLETLOO-----LVYDGSIVSEVLLRKESRN 129
Db 90 MEN--YVQWLQKLENIYVENKSEMAQIQNAVQNTATVLEIGTSLSTOT--ABQTRK 144
Qy 130 MNSRVQLVYNQLLHEIRKDNALSELQENRILNQTADMLQLASKYKYLEHKY----- 183
Db 145 LTVETQVNLQTSRLLETQLNLSLTYKLEKQLQQTNEILTKHEKNSLLEHKILEMEK 204
Qy 184 -----QHATLANQSEITIAQLSEHQQRVPSARVPVQPPAPRVPYQPTYN 231
Db 205 HKEBLDTLKEEKENLQGLVSRQTFITLQLEKQLSRA----- 240
Qy 232 RIINOISTNEIOSDONLKVLPPLPTMPTLTS-----LPSPDKSGPMDCLQALE 283
Db 241 -----TNNSILLKQQLLEL-----MDTVHNLVSLCTEGVLLKGGKKEEKPRDCADVQ 291
Qy 284 DGHDTSSIVYVKEPENTRLMQWCDQRHDBGWTIVQRLDGSVNFRRWETTYKQFGNI 343
Db 292 AGFNKSGIYIYVNNKPPKPPKPPKPPKPPKPPKPPKPPKPPKPPKPPKPPKPPKPP 351
Qy 344 DGEYVGLENIYVLTGNGVYKLVLTVMEDSGKRVFVAFSPRLEPSEYKRLGRYGN 403
Db 352 SGYWLNDEFIATSRQWYLRLEIMDEGNRAVSQYDFH:GNQKQRYLTLKCHTGA 411
Qy 404 G--DSTWNGKQFTLLDHDVYTGNCNCHYKGGWYTAACHSNLNGWYFGGHRSR 461
Db 412 GQSSSLIHL-GADFSFKDADNDNCMKCALMLTGWMPDAGSPSLNMGFYTAGQNHGL 470
Qy 462 ODGYWAEPFGSGSLKXVMMIRP 487
Db 471 L-NGIKWHYFKGSPYSLSRTTMMIRP 495

RESULT 5
AGP2_HUMAN STANDARD; PRT; 496 AA.
ID AGP2_HUMAN
AC O15123; Q9NRR7; Q9P217;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-2 precursor (ANG-2).
GN ANGPT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Lung;
RX MEDLINE=97349327; PubMed=9204896;
RA Malsompiere P.C., Suri C., Jones P.F., Bartunkova S., Wiegand S.J.,
RA Radziejewski C., Compton D., McClain J., Aldrich T.H.,
RA Yancopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
RT angiogenesis."
RL Science 277:55-60(1997).
RP SEQUENCE FROM N.A. (ISOFORM 1).

```

Matches	149;	Conservative	86;	Mismatches	163	Indels	124;	Gaps	15;
QY	42	NEYKRAAGSODK-----	CTYTFVFPQQRATGALCVNSKEPYLENPRHK-----						86
Db	20	NNFRKASMDSIGKQYOVHGSCSYTFLLPEM----	DNCSSSSPPY--SNAVGRAPLEY						73
QY	87	-----OELETLNN-----	ELLK-----						120
Db	74	DDSVQRLQYLEINEMNTQMLKLENTIQDMKKEMWEIQANAVQGTAWMEIGTNLLN							133
QY	121	-----KILRKESHNNMSRVTQLYMLHETIRKDNALNELSOLENNRIINQTAADLQIA							173
Db	134	QTAEQTRKLTDEVAQVLN-QTTRELEQL-----	EHSISTKLEKQILIDQTSYINKIQ						185
QY	174	SKYKDLNHY-----	QHATLANHQSSEIIAQLEEHQCRVPSAPFVQ						215
Db	186	DKKSIFLEKRYLAMEDKHIIQIQSISKEKRDQYVLVSQNSIIIELEK-----							232
QY	216	PPAPAPRVYQEPYVRIINQISTNEFIQSQDNKLYLPP-PTMPPLTSLSPSSIDKSGP-							274
Db	223	-----KVTATVNNSVLQCKQHDL-----	NETVNNLLTMMSTSSNAKDP						272
QY	275	-----WRDQLALEQHDGHTSSIVYKPEPNTRLKQWCDQDHPFGQTVIQRALDGS							326
Db	273	VAKEDQISRDDAEVFKSGHTTNGIYTLTFPNSFELIKACDMEAGGGWTIIQRREDGS							332
QY	327	VNFFRWETYYQKFGSNIDGEYWLGLNFIWLTNCGNTKLVTMEDNSGRVYEPVAFASFL							386
Db	333	VDFQRTWKEKYKFGNPGSEYWLGNFEFVSQLTNQRVYLKHLKDWEGNAYSLYHFFYL							392
QY	387	EPFSEYKRLRLGRHYGNMGD-SFTWHNKGQTTLRDHDYVYTGNCAYQKGMWVYACAH							445
Db	393	SSEELNRYRLHLGLGTMKXKISSISQPNDSYDQNDKDCIKCSQMLTGMWFPACGP							452
QY	446	SNLNGVWYRGHYRSRYQDGYVMAFFRGSYSLLKVVYMWIRP							487
Db	453	SNLNGWYVFPQGVTKNF-NGIKWYMKSGSYSLKATTWIRP							493

RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kwarabayashi Y.,
 RA Sato S., Nishida T., Seki N., Ishikawa K.-I., Tabata S.,
 RT Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (K1A0001-K1A0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1.";
 RL DNA Res. 1:27-35(1994).
 RN (4)
 RP SEQUENCE FROM N.A., AND VARIANT GLY-269 DEL.
 RA Shan Z.X., Yu X.Y., Lin Q.Y., Pu Y.H., Tan H.H., Zheng M., Lin S.G.,
 RT "Human angiotensin II mRNA variant forms."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION, IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESENCHYME. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated.
 CC -1- MISCELLANEOUS: IT MAY HAVE A POTENTIAL THERAPEUTIC UTILITY SINCE
 CC IT CAN BE USED FOR SPECIFICALLY TARGETING TUMOR VASCULATURE OR FOR
 CC PROMOTING ANGIOGENIC PROCESSES IN CERTAIN ORGANS SUCH AS AN
 CC ISCHEMIC HEART.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 CC
 DR EMBL: U83508; AAB50557.1; -
 DR EMBL: D13628; BAA02793.2; ALT_INTT.
 DR EMBL: AB084454; BAB91325.1; -
 DR EMBL: AY121504; AAM81745.1; -
 DR EMBL: AY124380; AAM92271.1; -
 DR HSSP: P02671; 1FZD.
 DR Genew: HGNC:484; ANGPT1.
 DR MIM: 601667;
 DR GO: GO:0005102; F:receptor binding; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C_1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 KM Angiogenesis; Glycoprotein; Coiled coil; signal; Polymorphism.
 FT SIGNAL 1 15
 FT CHAIN 16 498
 FT DOMAIN 81 119
 FT DOMAIN 153 261
 FT DOMAIN 284 498
 FT DISULFID 286 315
 FT DISULFID 439 452
 FT CARBOHYD 92 92
 FT CARBOHYD 122 122
 FT CARBOHYD 154 154
 FT CARBOHYD 243 243
 FT CARBOHYD 295 295
 FT VARIANT 269 269
 FT Missing (in cell line T98G; may be due to
 FT exon skipping).
 FT /FTID=VAR_009940.
 SQ SEQUENCE 498 AA: 57513 MW: 505FA63AEF6BE920 CRC64;
 21.3%; Score 572.5; DB 1; Length 498;

Best Local Similarity 29.4%; Pred. No. 1,7e-28;
 Matches 149; Conservativity 85; Mismatches 169; Indels 103; Gaps 15;
 QY 43 RYKAGSDQDCTTFTVPO-----QRTGALCVNSK-EP-----EVL 79
 DB 32 RYRIQHQ-CATYFLPEHDGNCRESTTDQYNTNALQDAPVDEDFSSQKQIHLHV 89
 QY 80 LENEHKOELLENLNLK-QKQIETLQO-----LVKVGIVSEVKLRKESRN 129
 DB 90 MEN--YQWQKLENYVENNKSEMAQIQNAQNHNTAMLEIGTSLSTQ---AEQTRK 144
 QY 130 MNSRTQIQVQLHETIRKDNALIELSQENRIINQADMLQLASKYKLEHY----- 183
 DB 145 LTVDETQVLMQTSRLIELQENSLSTYKLEKQIQETNELIKHEKNSLLEHKLMEGK 204
 QY 184 -----QHLATLANOSRIQLEHOCORVASRPVQPPAPRPVYQPTYN 231
 DB 205 HKELDLTKKEKELQGLVTRQYTIQELKQNLRA----- 240
 QY 232 RIINQISTNEIQSDQNLKVLPPPLTPMPTLS-----LPSTDKPSGPMWDCIQALE 283
 DB 241 -----TTNNSVLQKQLEL-----MDIVHNLVNLCTKEGVLLKGGKEEKEPFDCADVYQ 291
 QY 284 DGHDTSIYLVKENTRMLQWQCDQHDGSGMTVIQRILDSVNFRRMETYKQSGFNT 343
 DB 292 AGFKSGIYITTYNNPEPKVFCNMDVNGGQTVIQHREDGLDFQKGKEXMGFGNP 351
 QY 344 DGEYWGLENLYWLTQNGYKLLVTWEDWSGRKFAEYASFLRPESEYKRLGTYHGN 403
 DB 352 SGEWLGNERIFAITQQRQWMLRIELMDWEGNAYQYDFRFGHGNKQYRLYLKSHGT 411
 QY 404 AG--DFTWNGKQFTLDRDHVYTGNCANHYKGGWYTNACASHLNLGVTRGGHYRBR 461
 DB 412 AGQSSLIILH-GADFTKQDNDNCCKCALMLTGMPWDACGPNLNGMFTYAGQNHGK 470
 QY 462 YQDYVAEERFGSYSLKKVVMIRP 487
 DB 471 L-NGIKWHYKPSYSLRSTTWMIRP 495
 RESULT 7
 AGP4_MOUSE STANDARD; PRT; 509 AA.
 ID AGP4_MOUSE
 AC OSWVH6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiotensin-4 precursor (ANG-4) (ANG-3).
 GN ANGPT4 OR AGPT4 OR ANG3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Myoblasts, and Uterus;
 RX MEDLINE=9162530; PubMed=10051567;
 RA Valenzuela D.M., Griffiths J.A., Rojas J., Aldrich T.H., Jones P.F.,
 RA Zhou H., McElain J., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Huang T., Papadopoulos N., Maisonneuve P.C., Davis S.,
 RA Yancopoulos G.D.,
 RT Angiotensins 3 and 4: diverging gene counterparts in mice and
 RT humans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:1904-1909(1999).
 CC -1- FUNCTION: BINDS TO TYROSINE-PROTEIN KINASE RECEPTOR TIE2 AND MAY
 CC ACT AS AN ANTAGONIST.
 CC -1- SUBCELLULAR LOCATION: Secreted (probable).
 CC -1- TISSUE SPECIFICITY: Widely expressed.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -1- CAUTION: Was originally (Ref.1) called angiotensin-3.
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EMBL, AF113707; AAD21586.1; -
DR HSBP; P02671; 1F2D.
DR MGD; WGI:1336887; Agpt4.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KM Coiled coil; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 1 22 ANGIOPOIETIN-4.
FT DOMAIN 181 269 COILED COIL (POTENTIAL).
FT DOMAIN 294 480 FIBRINOGEN-LIKE.
FT DISULFID 297 326 BY SIMILARITY.
FT DISULFID 450 463 BY SIMILARITY.
SQ SEQUENCE 509 AA; 57805 MW; 9B5A74A20A6664F6 CRC64;

Query Match 20.8%; Score 558; DB 1; Length 509;
Best Local Similarity 29.1%; Pred. No. 1.4e-27;
Matches 154; Conservative 90; Mismatches 195; Indels 90; Gaps 16;

13 LLAAGVAGVGDGEFGTEGSPREFIYINRYKAGESODCTYTFITPQGRVAGIC-- 70
14 LLAATVAAAO---HRRGPAAGHROIHOVRR-----GQOSTYFVVRP---DICO 56
71 VNSKEPEVL-----LENRVKQDELLNNE--LTKQRQ 102
57 APTAPAPALGGSNSIQRDLPASRLHITWPAQRAQRAQVSGLEKLENNQMLTKES 116
103 I-----ETLQO---LYKVDGIVSEYKYLKESRNNSKVTQVMQLHEI 145
117 IKVNRSHLVQAQODITQNTTMTALGANLNQTK---AQCHKLTAVEAQVLTQTLHK 173
146 IKRDNALIELSQLENNILNQADMQLASKYDLEHKYQHLATLHNSSEITAOLEHCQ 205
174 TQMLNSLSTNKLKQMLKQSELRLOQRNALLETQALE--AQHQAG--LNSIQEKRE 230
206 RVPSARFVYQPPAPRPVYQPPYTRT---INQISTNEI---QSDQMLKVLPPPLTMP 259
231 QHSHLIG-----HQTGLANLKNHIALSSNSSSLQOQOQOCTEFVQRLVIV 278
260 TLTSLPSTDKSPGWDCLQMLEGHDHSSIVLVKPENTNRLMOWVCDQRHDPGWTVI 319
279 AODQHVSLSKTPKPVFQDCAETIKSGVNSVYTTIETMTKPLKVFCDMETDGGWTII 338
320 QRRLDGSVNFPRNWTYKQGFQGNIDGEVYLGLENTYMLTNOGNKYLVTMEDSGKXYFA 379
339 QRRDGSVNFPRNWTYKQGFQGNIDGEVYLGLENTYMLTNOGNKYLVTMEDSGKXYFA 398
380 EYASRFLPESESYKRLRGRYHGNAG--DSFTMHNGQFTTLRDYDTGNCAHQRKGM 438
399 QYENFOLGSEORYSLSVNDSSSSAKRKNSLAPQGRFTKMDNDNCCKCAQYLSGWM 458
439 WYNACGSHNLNGWYRGHYASRYODGVYWAFFRGSGSYLSKTYVMNIRP 487
459 WPDACGLSLNGLIY--SVNCHLKHNGIMHMFRRGSYSYLSHGRVWLRP 506

RESULT 8
AGP4 HUMAN STANDARD; PRT; 503 AA.
ID AGP4 HUMAN
16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiopoietin-4 precursor (ANG-4) (ANG-3).
GN ANGPT4 OR ANG4 OR ANG3.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=99232854; PubMed=10218486;
RA Nishimura M., Miki T., Yashima R., Yokoi N., Yano H., Sato Y.,
RA Seino S.;
RT "Angiopoietin-3, a novel member of the angiopoietin family.";
RT FEBS Lett. 448:254-256 (1999).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=99162530; PubMed=10051567;
RA Valenzuela D.M., Griffiths J.A., Rojas J., Aldrich T.H., Jones P.F.,
RA Zhou H., McClain U., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Huang T., Papadopoulos N., Maisonneuve P.C., Davis S.,
RA Yancopoulos G.D.;
RT "Angiopoietins 3 and 4: diverging gene counterparts in mice and humans.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:1904-1909 (1999).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill M.D., Butler A.P., Gardner C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hammond S., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Heath P.D., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.B., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasalho M.H., Leverisa M.A., Lloyd C., Lloyd D.W., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachle L.J., McKay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Senra H.K., Shownkeen R., Sims S.,
RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Suston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RT Nature 414:865-871 (2001).
[4]
RP FUNCTION: BINDS TO TYROSINE-PROTEIN KINASE RECEPTOR TIES2 AND
ACTIVATES IT.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE LUNG WITH MUCH LOWER
LEVELS FOUND IN OTHER TISSUES.
CC -1- CAUTION: Was originally (Ref.1) called angiopoietin-3.
CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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or send an email to license@isb-sib.ch).

EMBL; AF074332; AAD31728.1; -
EMBL; AF113708; AAD21587.1; -
EMBL; AL161939; CAC09933.1; -
DR HSBP; P02671; 1F2D.
DR Genew; HGNC:487; ANGPT4.

SO SEQUENCE 312 AA; 36391 MW; 26BC82124E660C2 CRC64;
 Query Match 20.0%; Score 537; DB 1; Length 312;
 Best Local Similarity 39.6%; Pred. No. 1.5e-26;
 Matches 111; Conservative 40; Mismatches 89; Indels 40; Gaps 9;

QY 232 RIINDISTNEIQ-----SDQNTKVLPPPLPTMTLTLSPSSDCKSGFPRDCLQALBQHD 287
 DB 50 KIKQLOENBVOFLKGDEN-----TVIDLGSKQ-----YADCEIFNDGYK 92
 QY 288 TSSILVLPENTNRLMQWCCQRRHDPGGTIVICRLDSVSPFFRWYKYGFGNI---D 344
 DB 93 LSGFKIKRPLQSPAFPSYCDM-SDGSGMTVYQKSDSENFNKMGKDYENGFKNFYQKH 151
 QY 345 GEYMLGLENIYVLTNGCNKLVLTWEDMSGRKFAEVAFLPESEYKRLGRYHNA 404
 DB 132 GEYMLGNKTLHFLTTOEDYTLKIDLADPEKNSRYAQYKXGDEKNFYELNIGYSGTA 211
 QY 405 GDSFT-----N-HNGKQFTLLDRPHDYVTGNCAYQKGGWYNAKAHSLNNGVY 453
 DB 212 GDSLGNFPEYQWNAHQMKFSTWDRDHDYEGNCAEEDQSGWGFRCISANLNGVY 271
 QY 454 RGHYRSRYQDGVYNAEPRGSGYSLLKRYVMYMRPN---PN 490
 DB 272 -SGPYTAKTDNGIWMYTHGMWYSLKSVYMKIRPNDFTPN 310

RESULT 10
 AGP2_PIG STANDARD; PRT: 496 AA.
 AC Q9BD7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiopoietin-2 precursor (ANG-2).
 GN ANGPT2;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1];
 RP MEDLINE FROM N.A. Pubmed=11230987;
 RX MEDLINE=21153163;
 RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.J., Koh G.Y.;
 RT "The angiopoietin-tie2 system in coronary artery endothelium prevents
 oxidized low-density lipoprotein-induced apoptosis.";
 RL Cardiovasc. Res. 49:872-881(2001).
 CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
 MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
 BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
 AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
 INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
 REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
 CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
 ANGIOGENIC SIGNAL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC EMBL; AF233228; AAK14993.1; -
 DR HSSP; P02671; 1FZD.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C; 1.
 DR SMART; SMO0186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
 KW Angiogenesis; Glycoprotein; Coiled coil; signal.

FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 496 ANGIOPOIETIN-2.
 FT DOMAIN 130 255 COILED COIL (POTENTIAL).
 FT DOMAIN 280 496 FIBRINOGEN C-TERMINAL.
 FT DISULFID 284 313 BY SIMILARITY.
 FT DISULFID 437 450 BY SIMILARITY.
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 496 AA; 56911 MW; 33802BE224FE6B9D CRC64;

Query Match 20.0%; Score 537; DB 1; Length 496;
 Best Local Similarity 28.1%; Pred. No. 2.6e-26;
 Matches 141; Conservative 95; Mismatches 182; Indels 84; Gaps 12;

QY 42 NRYKAGESQDK-----CTYFVLVQ-----QRYTGAICVNSKEPEVLLNRYHKE 88
 DB 20 NRPKMSDSTGKQYQVGHPCSTYFLPETNCRSPSSSYSAVQADPLDYDSVRR 79
 QY 89 LELINN-----ELK-----OKROIETQLVKYDGGIVSEV----- 120
 DB 80 LOVLENNIMENNTQWLMLESYIODNMKEWEVEIQQNAVQNTAVMLEIGTNLLNQABQT 139
 QY 121 -KILKESRMNNSRVQVQWQLHEIRKRDNALETQLENRLINQTDMLQALSKYKDL 179
 DB 140 RKLTDVBAQVILN-OTYIELQL-----EHSITKLEKQILDDTSEINKQDKNSFL 191
 QY 180 EHKYQHLATLANQSEIIIALEHQVPSFARVPQPPAPPRVQPPYVYKRIINDIST 239
 DB 192 EKYVLDMEDKHIVQLQSIKEKQDLQVIVSKQ-----NSLIEELK 232
 QY 240 NEISQDQIKLPP-----LPTVPTLSLSSDTPSGP-----WRDCLQALDGH 286
 DB 233 QLVATVYNSVLRQHQHDMETVHNLLMTSTNSAHSVLAKSEQILFRDCAEAFKSGL 292
 QY 287 DTSSIVLVKRPENTNRLMQWCCQRRHDPGGTIVICRLDSVSPFFRWYKYGFGNIDG 346
 DB 293 TTSQGYTLTFPNSIEETKAYCDMETGGGWTVIQRRDGSYDFQRTWKEYWYMGFSPSGE 352
 QY 347 YMLGLENYVLTNGCNKLVLTWEDMSGRKFAEVAFLPESEYKRLGRYHNA 406
 DB 353 HMLGHEFYSQVYTNQRYVLTKLHLDWEGNEAVSYLHEHYLSSSEFNRIHLKGLTGAK 412
 QY 407 -SFTWNGKQFTLLDRPHDYVTGNCAYQKGGWYNAKAHSLNNGVYRGHYRSRYQDG 465
 DB 413 ISSISQPNDSITGDADNDKICQSQMLTGGMWFDACGPNLNGMYYPQQRQNTKFG-NG 471
 QY 466 YMAEPRGSGYSLLKRYVMYMRPN 487
 DB 472 IKWYMKSGYSLLKATMMIRP 493

RESULT 11
 AGP1_BOVIN STANDARD; PRT: 481 AA.
 AC O18920;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiopoietin-1 precursor (ANG-1) (Fragment).
 GN ANGPT1 OR ANG1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=99054348; Pubmed=9840613;

RA Geede V., Schmidt T., Kimmina S., Kozian D., Augustin H.G.;
 RT "Analysis of blood vessel maturation processes during cyclic ovarian
 RL angiogenesis.";
 RN Lab. Invest. 78:1385-1394(1998).
 RP SEQUENCE OF 91-200 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=86451564; PubMed=976732;
 RA Mandriote S.J., Pepper M.S.;
 RT "Regulation of angiopoietin-2 mRNA levels in bovine microvascular
 RL endothelial cells by cytokines and hypoxia.";
 CC Circ. Res. 83:852-859(1998).
 CC -1- FUNCTION: BINDS AND ACTIVATES TIE2 RECEPTOR BY INDUCING ITS
 CC TYROSINE PHOSPHORYLATION. IMPLICATED IN ENDOTHELIAL DEVELOPMENTAL
 CC PROCESSES LATER AND DISTINCT FROM THAT OF VEGF. APPEARS TO PLAY A
 CC CRUCIAL ROLE IN MEDIATING RECIPROCAL INTERACTIONS BETWEEN THE
 CC ENDOTHELIUM AND SURROUNDING MATRIX AND MESSAGES. MEDIATES BLOOD
 CC VESSEL MATURATION/STABILITY. IT MAY PLAY AN IMPORTANT ROLE IN THE
 CC HEART EARLY DEVELOPMENT (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian
 CC cycle.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF093573; AAC61872.1; -;
 DR EMBL: AF032923; AAC78245.1; -;
 DR HSSP: P02671; IFZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C.1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR Angiogenesis; Glycoprotein; Coiled coil; signal.
 KW Angiogenesis; Glycoprotein; Coiled coil; signal.
 FT SIGNAL 1 15
 FT CHAIN 16
 FT DOMAIN 153 >481 ANGIOPOIETIN-1.
 FT DOMAIN 283 >481 COILED COIL (POTENTIAL).
 FT DISULFID 285 314 FIBRINOGEN C-TERMINAL.
 FT DISULFID 438 451 BY SIMILARITY.
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT NON_TER 481
 SQ SEQUENCE 481 AA; 55556 MW; 88EC9ED84FC2B850 CRC64;
 Query Match 20.0%; Score 536.5; DB 1; Length 481;
 Best Local Similarity 28.5%; Pred. No. 2.7e-26;
 Matches 146; Conservative 86; Mismatches 186; Indels 95; Gaps 16;
 QY 14 LAAMGAVAGQEDGFEETGEGSPREFIYARRYKAGESQDKCTYFIYPO-----QRTG 67
 DB 10 LAAILTHIGSNQSRSPENGG-----RRYRRIQHOG--CAYFIIPENHNGRESEITD 60
 QY 68 AICVNSKE---PEV-----LLENRYHKOELLLNNELIK-QKQIETTLQO- 108
 DB 61 QYNTNALORDAPHEQDPSQKOLHEHVMEN--YTOWLQKIENYIYENKSEMAQIQON 118
 QY 109 -----LVKVDGIVSEVKILKRESNNKMSRVTOYLMCLHILIKRDVALLESTLEN 160
 DB 119 AVQNHATMLETIGSLISLTQ---AEQTKLTDVETQVNLQNSRLIEQLLENSLSTYKLEK 175
 QY 161 RILNQTADMLQSLASYKDLHEKY-----QHLATLHNSQSELIAGLEE 202
 DB 176 QLLQCTNEILIKLHKENSLLEKIFEMEGKHKEIDTLKEKENIQGLVTSQTYIIQLEK 235

QY 203 HQQVPSARVPYPPAPPPAPPPVYQPTYNRIINOISTNEIQSDNKLKVLPPPLPTMPTLT 262
 DB 236 QLNATITNSVLQ-----KQLEMDIVYHNLVN-LCKREV----- 269
 QY 263 SLPSSTDXPSGPMWDCIQALEGDHSTSIYLVKENTRLMQWCQDRHDPGCVTVIQR 322
 DB 270 LLKGGKREKEKPPFDCAVDYQAGFNKSGIYIYINNPEPKVFCDDMDLNGGGTVIQR 329
 QY 323 LDGVSFPRMWEYTKQSGFNIDGMYLGLNIVYLTNQGNYKLLVTMDEMSGRKVPFEYA 382
 DB 330 EDGSLDQKQKKEIKMGFGNPSGSEYMLGNEFIFATISQROTYRIELLDWEGNAYSQYD 389
 QY 383 SFRLPESEYKYLGLRYHGNAG--DSFTWANGKQFTTLDRHDHYTGNCAYHOKGWMY 440
 DB 390 RFHIGNKQVRYLKLKHTGTAGKOSLIDH-GADFSTKXADNDNCMKCALMTGGWVF 448
 QY 441 NAGASHNLNGVWYGGHYRERYQDGVYMAFRG 473
 DB 449 DACGSPNLNGMFTYAGNHGKL-NGIKWHYFKG 480
 RESULT 12
 AGP2_MOUSE STANDARD; PRT; 496 AA.
 ID AGP2_MOUSE
 AC O35608; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
 GN ANGPT2 OR AGPT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=97349327; PubMed=9204896;
 RA Matsunier P.C., Suri C., Jones P.F., Barunkova S., Wiegand S.J.,
 RA Radziejewski C., Compton D.L., McClain J., Aldrich T.H.,
 RA Papadopoulos N., Daly T.J., Davis S., Sato T.N., Yancopoulos G.D.;
 RT "Angiopoietin-2, a natural antagonist for Tie2 that disrupts in vivo
 RT angiogenesis.";
 RL Science 277:55-60(1997).
 CC -1- FUNCTION: BINDS TO TIE2 RECEPTOR AND COUNTERACTS BLOOD VESSEL
 CC MATURATION/STABILITY MEDIATED BY ANGIOPOIETIN-1. ITS FUNCTION MAY
 CC BE CONTEXT-DEPENDENT. IN THE ABSENCE OF ANGIOGENIC INDUCERS, SUCH
 CC AS VEGF, ANG2-MEDIATED LOOSENING OF CELL-MATRIX CONTACTS MAY
 CC INDUCE ENDOTHELIAL CELL APOPTOSIS WITH CONSEQUENT VASCULAR
 CC REGRESSION. IN CONCERT WITH VEGF, IT MAY FACILITATE ENDOTHELIAL
 CC CELL MIGRATION AND PROLIFERATION, THUS SERVING AS A PERMISSIVE
 CC ANGIOGENIC SIGNAL.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed only at sites of vascular
 CC remodeling.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF004326; AAB63189.1; -;
 DR HSSP: P02671; IFZD.
 DR WGI: WGI1202890; Aspct2.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; Fibrinogen_C.1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.

KM Angiogenesis; Glycoprotein; Coiled coil; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 496
 FT DOMAIN 159 256
 FT DISULFID 280 496
 FT DISULFID 284 496
 FT DISULFID 437 496
 FT CARBOHYD 89 496
 FT CARBOHYD 119 496
 FT CARBOHYD 133 496
 FT CARBOHYD 151 496
 FT CARBOHYD 240 496
 FT CARBOHYD 304 496
 SQ SEQUENCE 496 AA; 56616 MW; FA3021FE4E01C410 CRC64;

Query Match 19.9%; Score 535.5; DB 1; Length 496;
 Best Local Similarity 28.9%; Pred. No. 3.3e-26;
 Matches 144; Conservative 82; Mismatches 163; Indels 109; Gaps 15;

QY 54 CTYTFVPOQRTGALCVNSKEPVLLEKHK-----QELSLNN-----EL 96
 DB 41 CYSYFLPPT-----DSCRSSSP--YMSNAVQRDAPLDYDSVQRLQVLENNLTOWL 94
 QY 97 LK-----OKROETLQOLVYKVDGIVSEV-----KLKESRNNNSRV 134
 DB 95 MLENYIQNMKEKWEIQNVQNTAVMIEIGSLNQTAQTRKLDVDAQVLA-QT 153
 QY 135 TOLVQNLHEIRKRDNALELSQENRIINOTADMQLASKYKDLBKX----- 183
 DB 154 TRLEQLT-----CHSISTWLEKQILDQTSINKONKNSFLEQKYLDMEGHSEQL 206
 QY 184 -----QHLATLANQSEIIAQLQEHQORVPSARVPQPPAAPRVYQPTVRIINQ 236
 DB 207 QSMKEQKDELQVLSKQSSVIDELE---KKLVTA-----TVNSLIQ 245
 QY 237 ISTNEIQSDQNLKVLPPPLPTPLTSLPSSTD-----KPSGPMWDLQALDEGHDTSS 290
 DB 246 KQOQDLMEIVN-----SLTWMSPNKSSVARIKEQOTFRDCAIEFKSGLTSSG 296
 QY 291 IYLVKPENNRLMQVWCQDRHDPGQWTVQRLDGSVNFRRWETVYKQFGINDSEYWG 350
 DB 297 IYLVKPENNRLMQVWCQDRHDPGQWTVQRLDGSVNFRRWETVYKQFGINDSEYWG 356
 QY 351 LENIYVLTQNGYKYLVTWEDWSGRKVPFAEYASFRLPESEYKYLRLGTHNAGD-SFT 409
 DB 357 NEFVSGSLTQOHRYVLAIKQIKDWEQNFASHLYDHFTYLAQESNVR.IHLTGLTGTAKISSI 416
 QY 410 WENGRQFTLDRDHVYTGNCAYQKGGWYNACAHNSNNGVYRGHRSRYQGVYWA 469
 DB 417 SQPGSFSFTRSDNDNDKICCKSCQMLSGGWFPACGSPNINQYQKONTNKF-NGIKWY 475
 QY 470 BFRGGSYSLKVVYMMRP 487
 DB 476 YMKGSYSLKATMMIRP 493

RESULT 13
 FIBB BOVIN STANDARD; PRT; 468 AA.
 AC P02676;
 DT 21-UTL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN FGB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE OF 1-4.
 RA Blomback B., Doolittle R.F.;

RT "The sequence of amino acids at the N-terminal end of bovine
 RT fibrinopeptide B.";
 RL Acta Chem. Scand. 17:1816-1819(1963).
 RN [2]
 RP SEQUENCE OF 5-21.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides.";
 RL Ark. Kent 16:425-436(1960).
 RN [3]
 RP SEQUENCE OF 22-53.
 RX MEDLINE=79164394; PubMed=434821;
 RA Martindale R.A., Ingles A.S., Rubira M.R., Hageman T.C.,
 RA Hurrell J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 RT bovine fibrinogen.";
 RL Arch. Biochem. Biophys. 192:27-32(1979).
 RN [4]
 RP SEQUENCE OF 44-468 FROM N.A.
 RX MEDLINE=81199473; PubMed=6262803;
 RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of a cDNA clone coding for the beta chain of bovine
 RT fibrinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470(1981).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot. The soft clot is converted
 CC into the hard clot by factor XIIIa which catalyzes the epsilon-
 CC (gamma-glutamyl)lysine cross-linking between gamma chains
 CC (stronger) and between alpha chains (weaker) of different
 CC monomers.
 CC -1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC
 CC EMBL: V00110; CAA23444.1; -.
 CC PDB: 1JY2; 22-MAY-02.
 CC PDB: 1JY3; 22-MAY-02.
 CC InterPro: IPR002181; Fibrinogen_C.
 CC Pfam: PF00147; fibrinogen_C; 1.
 CC SMART: SM00186; FBC; 1.
 CC PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
 CC Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation;
 CC Pyridoxal carboxylic acid; 3D-structure.
 CC PEPTIDE 1 21
 CC CHAIN 22 468
 CC MOD RES 1 1
 CC MOD RES 6 6
 CC SITE 21 22
 FT DISULFID 72 72
 FT DISULFID 83 83
 FT DISULFID 87 87
 FT DISULFID 200 200
 FT DISULFID 204 204
 FT DISULFID 208 293
 FT DISULFID 218 247
 FT DISULFID 401 414
 FT CARBOHYD 371 371
 SQ SEQUENCE 468 AA; 53340 MW; 2DEDA2F443AA4B37 CRC64;

Query Match 19.6%; Score 527.5; DB 1; Length 468;

RP X-RAY CRYSTALLOGRAPHY (2.3-ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands".
RL Biochemistry 37:8637-8642(1998).
RN [16]
RN X-RAY CRYSTALLOGRAPHY.
RP MEDLINE=99175069; PubMed=10074346;
RX Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RA "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide".
RL Biochemistry 38:2941-2946(1999).
RN [17]
RP INTERACTION WITH FELTN.
RX MEDLINE=95370264; PubMed=7642629;
RA Tian H., Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
RA Argaves W.S.;
RT "The interaction of fibrulin-1 with fibrinogen. A potential role in
RT hemostasis and thrombosis".
RL J. Biol. Chem. 270:19458-19464(1995).
RN [18]
RP VARIANT BALTIMORE-2 LYS-478.
RX MEDLINE=89058942; PubMed=3194892;
RA Schmeizel C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
RT structural studies of fibrinogen Baltimore II".
RL Thromb. Res. 52:173-177(1988).
RN [19]
RP VARIANT ISE ARG-45.
RX MEDLINE=91208409; PubMed=2018936;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RA Asakura S., Shirakawa S.;
RT "A new congenital abnormal fibrinogen Ise characterized by the
RL replacement of B beta glycine-45 by cysteine".
RL Blood 77:1958-1963(1991).
RN [20]
RP VARIANT NAPLES THR-98.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Havrlikte F., Lord S.T., Grimbergen J., Mannucci P.M.;
RT "Molecular basis of fibrinogen Naples associated with defective
RT thrombin binding and thrombophilia. Homozygous substitution of B beta
RT 68 Ala-->Thr".
RL J. Clin. Invest. 90:238-244(1992).
RN [21]
RP VARIANTS IJMUJIDEN CYS-44 AND NIJMEGEN CYS-74.
RX MEDLINE=92228809; PubMed=1565641;
RA Koopman J., Havrlikte F., Grimbergen J., Engesser L., Novakova I.,
RA Kerst A.F.J.A., Lord S.T.;
RT "Abnormal fibrinogens IjmuJiden (B beta Arg14-->Cys) and Nijmegen (B
RT beta Arg44-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes".
RL Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482(1992).
RN [22]
RP VARIANT NEW YORK-1 39-GLY--LEU-102 DEL.
RX MEDLINE=85157605; PubMed=3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional
RT fibrinogen with a deletion of B beta(9-72) corresponding exactly to
RT exon 2 of the gene".
RL J. Biol. Chem. 260:4390-4396(1985).
RN [23]
RP VARIANTS GLU-2; LEU-265 AND LYS-478.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargili M., Althuler D., Itzland J., Sklar P., Arlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanasaman N., Nimesh U., Zhang L.,
RA Fierland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes".
RL Nat. Genet. 22:231-236(1999).
RN [24]
RP ERRATUM.

RA Cargill M., Altschuler D., Ireland U., Sklar P., Ardle K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.O.,
RA Lander E.S.,
RL Nat. Genet. 23:373-373(1999).

RN [25]
RP VARIANTS CONGENITAL AFIBRINOGENEMIA ARG-383 AND ASP-430.
RX MEDLINE=20129589; PubMed=1066208;
RA Dua S., Asselta R., Santagostino E., Zeinali S., Simonic T.,
RA Malcovati M., Mannucci P.M., Tenchini M.L.;
RT "Missense mutations in the human beta fibrinogen gene cause
congenital afibrinogenemia by impairing fibrinogen secretion."
RL Blood 95:1336-1341(2000).
RN [26]
RP VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.
RX MEDLINE=21361164; PubMed=11468164;
RA Lounes K.C., Leikowitz J.B., Henschel-Ekman A.H., Coates A.I.,
RA Hartgen R.R., Lord S.T.,
RT "The impaired polymerization of fibrinogen longmont

Query Match 19.6%; Score 526.5; DB 1; Length 491;
Best Local Similarity 30.3%; Pred.No.1.2e-25;
Matches 138; Conservative 64; Mismatches 114; Indels 139; Gaps 16;

OY 92 LNNELLQKROIEFLQOLVKYDGVISEVKKLRRESRMASRYQL-----YNQLLHEI 145
DB 112 LOEALLQOEIRFN-----SVD-----ELNNVAEAVQTSSSFQYWLILDL 154
OY 146 IRKRDNALE-----LSOLENRIL-----NCTADMLQASKYDLEHKYQHAT 188
DB 155 WKQKQKOVKNENNVNNEYSELEHQYLIDETVANSIPTRNLARVLISLENRSKIQL-- 212
OY 189 LAHNSSETIALGEEHCORVPSPARPPOPPAPPRVYQPTYYNRITINOSTNEIOSDONL 248
DB 213 -----ESVSAQM--EYC-RTPCT-----VSGR----- 232
OY 249 KYLPPLPLEMTTLTSLPSSTDKPSPMRDCQLALEGDHDTSSIVLYRENNTRLMWQCWD 308
DB 233 ----PVV-----SG--KECEILLRKGETSETEMLIQPDSSVKPYRVCD 271
OY 309 QRHDPGGTVIQRRLDGSVNFFRWETKYOGFNI-----DEGYWLGENTYW 356
DB 272 MNTENGGMVTIVQNQDDGSVDGRKMDPKQGFGVAVATWTDDKNYGCLGEYWLGNDKISQ 331
OY 357 LTNGNYKLVTMEDWSGRKVFABAYASRLPEBSEYTKLRIGRIYGNAGD----- 406
DB 332 LTRMGPELLILEMDEWKDGFKYAHYGGFTQVENANKYOISVYKRYGTXGLMALDGAQLM 391
OY 407 ----SFWNHNGKOFTTLDRDHEDVTGN-----CAHYCKGWMYVACAHSNLNGVMYRGSH 457
DB 392 GENRTMIHNGMFSTYDRDNDGHLTSIPRKCQKEDGGGWYNRCHAAANPGRIRYWGSG 451
OY 458 Y----RSRYODGYVWAEFRCGYSLLKKVVMIRP 487
DB 452 YTMDAKHGHTDDGVVMMWMKGSWYSMRKMSXKIRP 486

RESULT 15
FIBA_CHICK STANDARD; PRT; 741 AA.

ID FIBA_CHICK AC
AC P14448;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha-B chain precursor [contains: Fibrinopeptide A].
GN FGA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archaeosuria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC Gallus.
NCBI_Taxid=9031;
LN [1]
RP SEQUENCE OF 1-4 FROM N.A.


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Db 61 POORVTGALCVNSKEPEVHLNENRHKQELINNELKQKQIETLQOLVEVDGIVSEV 120
QY 121 KILRKESRRNNNSRVTLQYMLLHEIIRKDNALLETSOLENRILNQTADMLQLASKYKYLE 180
Db 121 KILRKESRRNNNSRVTLQYMLLHEIIRKDNALLETSOLENRILNQTADMLQLASKYKYLE 180
QY 181 HKYOHATLTAHNOSEIIAOLEEHQORVPASRPVOPPPAPPRVYQPTYNRIINQISTN 240
Db 181 HKYOHATLTAHNOSEIIAOLEEHQORVPASRPVOPPPAPPRVYQPTYNRIINQISTN 240
QY 241 EIOSDONLKYLPPLPTMPTLSLPSSTDKPSGPMWDCIQALEDGHTSSIYLVPKENTN 300
Db 241 EIOSDONLKYLPPLPTMPTLSLPSSTDKPSGPMWDCIQALEDGHTSSIYLVPKENTN 300
QY 301 RLMQVWCDDQHDHDPGWTVIQRRLDGSVNFPRNMEYTKQGFNIDGEMVLGLENIYMLTNQ 360
Db 301 RLMQVWCDDQHDHDPGWTVIQRRLDGSVNFPRNMEYTKQGFNIDGEMVLGLENIYMLTNQ 360
QY 361 GNYKLIVTMEDWSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
Db 361 GNYKLIVTMEDWSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAYHQKGGWYTNACAHSNLNGVWYRGHYSRYQDGYVMAEFRGGSYLK 480
Db 421 RDHDVYTGNCAYHQKGGWYTNACAHSNLNGVWYRGHYSRYQDGYVMAEFRGGSYLK 480
QY 481 VMMIRPNPTFH 493
Db 481 VMMIRPNPTFH 493

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RESULT 2
ID 09J03 PRELIMINARY; PRT; 493 AA.
AC 09J03;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Angiotensin II type 1A receptor associated protein.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar-Kyoto; TISSUE=Vascular smooth muscle;
RA Guo D.F., Baranes D., Ono Y., Porter J.P., Abi-Jaoude E., Orlov S.N.,
RA Inagami T.;
RT "ARAP1 is required for recycling and resensitization of angiotensin II
RT type 1A receptor."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159049; AAF80364.1; -.
DR HSSP; P02671; 1FZD.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; Fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KM Receptor.
SQ SEQUENCE 493 AA; 57159 MW; 7C37652C472B2341 CRC64;

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Query Match 94.8%; Score 2546; DB 11; Length 493;
Best Local Similarity 94.5%; Pred. No. 66-170;
Matches 466; Conservative 9; Mismatches 18; Indels 0; Gaps 0;
QY 1 MRPPLCVTGMWLGILAMGAVAGQEDGFEGTSGPREFYINRYRAGESODKCTYPTIV 60
Db 1 MRPPLCVTGMWLGILAMGAVAGQEDGFEGTSGPREFYINRYRAGESODKCTYPTIV 60
QY 61 POORVTGALCVNSKEPEVHLNENRHKQELINNELKQKQIETLQOLVEVDGIVSEV 120
Db 61 POORVTGALCVNSKEPEVHLNENRHKQELINNELKQKQIETLQOLVEVDGIVSEV 120

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QY 121 KILRKESRRNNNSRVTLQYMLLHEIIRKDNALLETSOLENRILNQTADMLQLASKYKYLE 180
Db 121 KILRKESRRNNNSRVTLQYMLLHEIIRKDNALLETSOLENRILNQTADMLQLASKYKYLE 180
QY 181 HKYOHATLTAHNOSEIIAOLEEHQORVPASRPVOPPPAPPRVYQPTYNRIINQISTN 240
Db 181 HKYOHATLTAHNOSEIIAOLEEHQORVPASRPVOPPPAPPRVYQPTYNRIINQISTN 240
QY 241 EIOSDONLKYLPPLPTMPTLSLPSSTDKPSGPMWDCIQALEDGHTSSIYLVPKENTN 300
Db 241 EIOSDONLKYLPPLPTMPTLSLPSSTDKPSGPMWDCIQALEDGHTSSIYLVPKENTN 300
QY 301 RLMQVWCDDQHDHDPGWTVIQRRLDGSVNFPRNMEYTKQGFNIDGEMVLGLENIYMLTNQ 360
Db 301 RLMQVWCDDQHDHDPGWTVIQRRLDGSVNFPRNMEYTKQGFNIDGEMVLGLENIYMLTNQ 360
QY 361 GNYKLIVTMEDWSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
Db 361 GNYKLIVTMEDWSGRKVFAYASFRLEPSEYKRLGRYHGNAGDSFTWNGKQFTTLD 420
QY 421 RDHDVYTGNCAYHQKGGWYTNACAHSNLNGVWYRGHYSRYQDGYVMAEFRGGSYLK 480
Db 421 RDHDVYTGNCAYHQKGGWYTNACAHSNLNGVWYRGHYSRYQDGYVMAEFRGGSYLK 480
QY 481 VMMIRPNPTFH 493
Db 481 VMMIRPNPTFH 493

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RESULT 3
ID 095841 PRELIMINARY; PRT; 491 AA.
AC 095841;
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Angiotensin Y1 (DJS95C2.2) (Angiotensin-related protein 1 precursor)
DE (Angiotensin-like 1).
GN DJS95C2.2 OR ARP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Kim T., Kwak H.-J., Ahn J.E., So J.N., Liu M., Koh K.N., Koh G.Y.;
RT "Molecular cloning and characterization of a novel angiotensin family
RT protein, angiotensin-3."
RL FEBS Lett. 443:353-356 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cobley V.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ota T., Nishikawa T., Kawai Y., Suzuki Y., Ishii S., Saito K.,
RA Yamamoto J., Sugano S., Isogai T.;
RT "HRI human cDNA sequencing project."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ito Y., Oike Y., Yasunaga K., Matsumoto S., Ota T., Nishikawa T.,
RA Kawai Y., Isogai T., Hamada K., Saito Y., Miyata K., Masuno Y.,
RA Suda T.;
RT "Molecular cloning and characterization of novel angiotensin-related
RT protein (ARP4)."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [5]

```

RP SEQUENCE FROM N.A.
 RC Tissue=Ovary;
 RA Strusberg R;
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF107253; AAD19608.1; -
 DR EMBL; AL355520; CAC13169.1; -
 DR EMBL; AB056476; BAB40691.1; -
 DR EMBL; BC050640; AAB50640.1; -
 DR HSP; P02671; IFZD.
 DR GO; GO:0005102; F-acceptor binding; TAS.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF0147; Fibrinogen_C_1.
 DR SMART; SM0186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR Signal.
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 481 POTENTIAL.
 SQ SEQUENCE 491 AA; 56719 MW; 3C4DBDE6CF7E99 CRC64;
 Query Match 56.1%; Score 1507.5; DB 4; Length 491;
 Best Local Similarity 58.6%; Pred. No. 2.8e-97;
 Matches 290; Conservative 69; Mismatches 109; Indels 27; Gaps 9;

QY 9 WVLGLIANGAAGVAGDEGEFEGEGSPREF---IYLRKYRAGSOD---KCTYTFVP 61
 DB 6 WVLGLVFLLDVDTGHCRCG-----GQFKIKIKINQRYPRATDGKEAKKCAVTFVP 56
 QY 62 QQRVTAICVNSKEPEV-LLENRVHKOELINNELKOKROIEYIQQLVKVDGIVEV 120
 DB 57 EQRITPICVNTKGDASTIKMTIMEDENKDVLSRKEIDVLQVLVDGIVNEV 116
 QY 121 KILRESRNMSRVYQVQLHEITRKDNALISOLENRIINQADMLQASKYKDE 180
 DB 117 KILRKESRNMSRVYQVQLHEITRKDNALISOLENRIINQADMLQASKYKDE 176
 QY 181 HXYQHATLAHNOSEIACLEHCORVPARVPQPP---AAPRVYQPPYNNIINQI 237
 DB 177 VKYASITDLVNNOSVITLLEEOCLRIFSRQTHSPVLYQVVPQHI--PNSQYTPGLI 234
 QY 238 STNEISQDQNL--KVLPP-LPTMPTLT--SLPSSTDKSGPWRDCLQALDEGHDTSIY 292
 DB 235 GGNIEIQRDGVPRLDLPRLDPLATSPFKSPFKIPVTFINEGPFKCOQAKGHSVSGIY 294
 QY 293 LYKPEPTNLMQVQCQRHDPGWTYIQRELGSVNFNNMITYOGFENIDGFWLGE 352
 DB 295 MKRPENSGPMQWCENSIDPGWTVYQKRTGSAVNFNNMENYKKGFGNIDGFWLGE 354
 QY 353 NIYMLTNGQNYKLLVMEDESGKVPFAEYASFLPESESEYKLRIGRYHGNAGDSFTW 412
 DB 355 NIYMLTNGQNYKLLVMEDESGKVPFAEYASFLPESESEYKLRIGRYHGNAGDSFTW 414
 QY 413 GKQFTLDRDHDVYTGNCAYQKGGWVYNAACAHNSINNGVYRGHRSRYQGVYMAER 472
 DB 415 GKQFTLDRDHDVYTGNCAYQKGGWVYNAACAHNSINNGVYRGHRSRYQGVYMAER 474
 QY 473 GGSYSLKVVMTMP 487
 DB 475 GGSYSLRVQMMIKP 489

RESULT 4
 OBN2J9 TISSUE=Ovary;
 ID OBN2J9; PRELIMINARY; PRT; 236 AA.
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypochemical protein FLJ30545.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC Tissue=Ovarian carcinoma;
 RA Isogai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Nishimura K.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (Mar-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AK075026; BAC1358.1; -
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF0147; Fibrinogen_C_1.
 DR SMART; SM0186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR Hypochemical protein.
 KW Hypochemical protein.
 SQ SEQUENCE 236 AA; 27672 MW; CEE3AFA26CA12575 CRC64;
 Query Match 50.4%; Score 1353; DB 4; Length 236;
 Best Local Similarity 100.0%; Pred. No. 6.9e-87;
 Matches 236; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 MPTLTSPLSSSTDKSGPWRDCLQALDEGHDTSIYLYKPEPTNLMQVCDQHPDQGT 317
 DB 1 MPTLTSPLSSSTDKSGPWRDCLQALDEGHDTSIYLYKPEPTNLMQVCDQHPDQGT 60
 QY 318 VIQRRLGSAVNFNNMITYOGFENIDGFWLGLENIYMLTNGQNYKLLVMEDESGKV 377
 DB 61 VIQRRLGSAVNFNNMITYOGFENIDGFWLGLENIYMLTNGQNYKLLVMEDESGKV 120
 QY 378 FAEYASFLPESESEYKLRIGRYHGNAGDSFTWNGHGFLLDRDHDVYTGNCAYQK 437
 DB 121 FAEYASFLPESESEYKLRIGRYHGNAGDSFTWNGHGFLLDRDHDVYTGNCAYQK 180
 QY 438 WYNAACAHNSINNGVYRGHRSRYQGVYMAERGGSYSLKVVMMIRPNPTFH 493
 DB 181 WYNAACAHNSINNGVYRGHRSRYQGVYMAERGGSYSLKVVMMIRPNPTFH 236

RESULT 5
 OQC2Z8 TISSUE=Embryo;
 ID OQC2Z8; PRELIMINARY; PRT; 332 AA.
 AC OQC2Z8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 10 days embryo cDNA, RIKEN full-length enriched library,
 DE clone:2610304B20, full insert sequence.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamashita I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.T., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Nazarelli U., Nomaetsu P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitlaker C., Wilting L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;

Query Match 41.3%; Score 1110; DB 4; Length 191;
 Best Local Similarity 100.0%; Pred. No. 5.3e-70;
 Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 MOVWCDORRDPGQWTVIQRRLDGSVNFPMNMTYKQGFNGEYWLGLNENYMLTNGQ 362
 DB 1 MOVWCDORRDPGQWTVIQRRLDGSVNFPMNMTYKQGFNGEYWLGLNENYMLTNGQ 60

QY 363 YKLLVYTMEDWSGRKVFAEYAFLEPESYKLRIGRTHGNAGDSFTWNGKQFTLLDRD 422
 DB 61 YKLLVYTMEDWSGRKVFAEYAFLEPESYKLRIGRTHGNAGDSFTWNGKQFTLLDRD 120

QY 423 HGVYVNGCAHYKQKGMWYNAACHSNLNGVYRGHYSRKYODGYVMAEPFGGSYSLKKV 482
 DB 121 HGVYVNGCAHYKQKGMWYNAACHSNLNGVYRGHYSRKYODGYVMAEPFGGSYSLKKV 180

QY 483 MMIRPNPNTFH 493
 DB 181 MMIRPNPNTFH 191

RESULT 8
 Q8N199 PRELIMINARY; PRT; 470 AA.
 AC Q8N199;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ARP3.
 GN ARP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matsuno S., Saito Y., Masuho Y., Yasunaga K., Oike Y., Suda T.;
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oike Y., Suda T.;
 RT "Molecular cloning of ARP3.";
 RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB054064; BAB91248.1; -;
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C.1.
 DR SMART; SM00186; FBG.1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 470 AA; 51694 MW; FAD20B1B00965239 CRC64;

Query Match 40.7%; Score 1094.5; DB 4; Length 470;
 Best Local Similarity 46.3%; Pred. No. 2.1e-68;
 Matches 213; Conservative 73; Mismatches 147; Indels 27; Gaps 7;

QY 44 YKRAGESQDKCTYTFIVPQORVTGALCVNSKEPEVLLNRYKQELNELLKQKQOI 103
 DB 19 WARAQ--APRCTYTFVLPQKFTGAVCMGSPASTRATPEAANASBLALRMVGRHEELL 76

QY 104 ETLQOLVYVGGIVSEVKLRKESRNMSRYTQLYMQLHE-----IIRKDNAL 155
 DB 77 RELQRLAADAAGVAGVRAALRKESRGLSARLQGLRQLOHEHGPAGADGAEPPAAL 136

QY 156 SQLENRLINQADMLQSLAKYKDLNRYKQHLATLANQSEIILQLEHQRVPASRPVQ 215
 DB 137 ALIGERVLNASEAQAARFHLQDVKFRLEQLVTOQSSILARLERLCPGAGAGQOQVL 196

QY 216 PEPAPRPVYQPPRYNRIINQISTN-----EIQSDNKLKLPPLPTPTLSLPS 267
 DB 197 PEPPLPVV---PV--RLVGSSTSDTSRMLDPAEPQDQTOQOEPMASPM--AGHPAV 249

QY 268 TDKPSGWRDCLQALEDHGDTSSIYLVKPEPNTNRLMQWCDQHDHFGMTVIGRLDGSV 327

DB 250 PTKFVGPWQDCAEAPQAGHEQSGVYELRV--GHHVSVWCEQQLLEGGMVIGRQDGSV 307
 QY 328 NFFPNMWTYKQGFNGEYWLGLNENYMLTNGQYKLLVYTMEDWSGRKVFAEYAFLE 387
 DB 308 NFFTTQHYKAGFCRPRPGEYWLGLEPYQLTSGDHLLVLLHEDWGRGARAHYDGSLE 367

QY 388 PESSEYKLRIGRYGNAGDSFTWNGKQFTLLDRDHDVYTGCAHYKQKGMWYNAACHSN 447
 DB 368 PESDHYKLRIGRYGNAGDSFTWNGKQFTLLDRDHDVYTGCAHYKQKGMWYNAACHSN 427

QY 448 LNVYVNGCAHYKQKGMWYNAACHSNLNGVYRGHYSRKYODGYVMAEPFGGSYSLKKV 482
 DB 428 LNVYVNGCAHYKQKGMWYNAACHSNLNGVYRGHYSRKYODGYVMAEPFGGSYSLKKV 467

RESULT 9
 Q9B220 PRELIMINARY; PRT; 470 AA.
 ID Q9B220;
 AC Q9B220;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Angiotensin-related protein 5.
 GN ARP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Samal B., Wu C., Dias P., Singh S.;
 RT "Molecular cloning of a novel angiotensin-related protein.";
 RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF230330; AAK06404.1; -;
 DR HSSP; P02671; IFPD.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C.1.
 DR SMART; SM00186; FBG.1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 470 AA; 51693 MW; FD64AABDA6B6518F CRC64;

Query Match 40.6%; Score 1090.5; DB 4; Length 470;
 Best Local Similarity 46.1%; Pred. No. 4.1e-68;
 Matches 212; Conservative 74; Mismatches 147; Indels 27; Gaps 7;

QY 44 YKRAGESQDKCTYTFIVPQORVTGALCVNSKEPEVLLNRYKQELNELLKQKQOI 103
 DB 19 WARAQ--APRCTYTFVLPQKFTGAVCMGSPASTRATPEAANASBLALRMVGRHEELL 76

QY 104 ETLQOLVYVGGIVSEVKLRKESRNMSRYTQLYMQLHE-----IIRKDNAL 155
 DB 77 RELQRLAADAAGVAGVRAALRKESRGLSARLQGLRQLOHEHGPAGADGAEPPAAL 136

QY 156 SQLENRLINQADMLQSLAKYKDLNRYKQHLATLANQSEIILQLEHQRVPASRPVQ 215
 DB 137 ALIGERVLNASEAQAARFHLQDVKFRLEQLVTOQSSILARLERLCPGAGAGQOQVL 196

QY 216 PEPAPRPVYQPPRYNRIINQISTN-----EIQSDNKLKLPPLPTPTLSLPS 267
 DB 197 PEPPLPVV---PV--RLVGSSTSDTSRMLDPAEPQDQTOQOEPMASPM--AGHPAV 249

QY 268 TDKPSGWRDCLQALEDHGDTSSIYLVKPEPNTNRLMQWCDQHDHFGMTVIGRLDGSV 327
 DB 250 PTKFVGPWQDCAEAPQAGHEQSGVYELRV--GHHVSVWCEQQLLEGGMVIGRQDGSV 307

QY 328 NFFPNMWTYKQGFNGEYWLGLNENYMLTNGQYKLLVYTMEDWSGRKVFAEYAFLE 387
 DB 308 NFFTTQHYKAGFCRPRPGEYWLGLEPYQLTSGDHLLVLLHEDWGRGARAHYDGSLE 367

QY 388 PESSEYKLRIGRYGNAGDSFTWNGKQFTLLDRDHDVYTGCAHYKQKGMWYNAACHSN 447
 DB 368 PESDHYKLRIGRYGNAGDSFTWNGKQFTLLDRDHDVYTGCAHYKQKGMWYNAACHSN 427

QY 448 LAGVWYRGHYSRYODGYMAEPRGGSYSLKVVMMIRP 487
 DB 428 LAGVWYRGHYSRYODGYMAEPRGGSYSLKVVMMIRP 467

RESULT 10
 Q8R026 PRELIMINARY; PRT; 457 AA.

ID Q8R026; AC Q8R026; DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE Similar to angiotensin-related protein 5 (ARP3).
 GN 6330404E1R1K OR ARP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Watanabe S., Saito Y., Maehuo Y., Yasunaga K., Oike Y., Suda T.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Oike Y., Suda T.;
 RT "Molecular cloning of ARP3."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC025904; AAH25904.1; -;
 DR EMBL; AB054065; BAB91249.1; -;
 DR MGI; MGI:1917976; 6330404E1R1K.
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C_1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 SQ SEQUENCE 457 AA; 51095 MW; B7C4289E3FEC6C3E CRC64;

Query Match 36.7%; Score 987; DB 11; Length 457;
 Best Local Similarity 44.0%; Pred. No. 6.9e-61;
 Matches 195; Conservative 78; Mismatches 146; Indels 24; Gaps 7;

QY 53 KTYTFIVQGVNTAICNSKEPEVLENRHKELENNELKORQJETIQOLVKV 112
 DB 26 RCRVTLVSPQKATSAVCRSEATQ-----DSELATLWRGHEHLLRALQRAAE 77
 QY 113 DGGIVSEVLLKESRNMNSRYTQLYMQLHEIRKDNAL-----LSQLENTLINTAD 168
 DB 78 GGALADVRAUREHSLTINTRLGQLRAQLQGEARAPDLGAPPAALGLALRALDAE 137
 QY 169 MGLASKYKDLHFKYQHLATLANOSELILOLEHCOVPSARPVPPOPPAP---PRV 224
 DB 138 ARRTTARQQLDAQRLREHAOLMSCHSSLLGRLOACAPERGQOQVLPPLAPVPLSLV 197
 QY 225 YQPTFYNLIQISTNEIQSDNKLKLPPLPTMPT--LTSPPSSTDKSGPWRDQALE 283
 DB 198 GSASTSTRLQ--TPHQREGSLRQGPSPSLPTGLHAPT---RPGWNRCAAHG 252
 QY 284 DGHDTSSILYKPEENTLMQVCDQRHDPGGVITIQRLDGSVNFRRMETYKQGFNI 343
 DB 253 AGHMOGSGVADLR--LGRVIVAVMCEQOEGGGMTVIQRQDGSVNFRRMTHYVAGGRP 310
 QY 344 DGEVYLGLENITWLNQGNKYLLVTMEDSGRKVFAEYASRLPESEYKRLRGVHGN 403
 DB 311 ESEYVLGLPEVAVQVSRQDHELLILLEGWGAARAHDSLSLSESDHYRLRGVYHD 370
 QY 404 AGDSFTWNGKQFTLLDRDHDVYTGNCAYQKGGWYVYACAHSNLNGWYRGHYSRYQ 463
 DB 371 AGDSLSWNRKPEFSTVDRDSDYSNCALYHGGWYVYACAHSNLNGWYRGHYSRYQ 430
 QY 464 DGVYMAEPRGGSYSLKVVMMIR 486

DB 431 DGVYMAEPRGGSYSLKVVMMIR 453

RESULT 11
 Q8BMV1 PRELIMINARY; PRT; 200 AA.

ID Q8BMV1; AC Q8BMV1; DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Weakly similar to angiotensin Y1 (fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,776 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK027978; BAC25687.1; -;
 DR InterPro; IPR002181; Fibrinogen_C.
 DR Pfam; PF00147; fibrinogen_C_1.
 DR SMART; SM00186; FBG; 1.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 FT NON TER 1 1
 SQ SEQUENCE 200 AA; 22518 MW; E1FE92E20171F54 CRC64;

Query Match 34.6%; Score 929; DB 11; Length 200;
 Best Local Similarity 77.7%; Pred. No. 2.6e-57;
 Matches 153; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

QY 291 IYVKEENTRLMOWCDDQDRHDSGTIVYQRLDGSVNFRRMETYKQGFNIIDGYWIG 350
 DB 2 IYVKEENTRLMOWCDDQDRHDSGTIVYQRLDGSVNFRRMETYKQGFNIIDGYWIG 61
 QY 351 LENIYVLTQGNKYLLVTMEDSGRKVFAEYASRLPESEYKRLRGVHGNAGDSPTW 410
 DB 62 LDIYVLTQGNKYLLVTMEDSGRKVFAEYASRLPESEYKRLRGVHGNAGDSPTW 121
 QY 411 HNGKQFTLLDRDHDVYTGNCAYQKGGWYVYACAHSNLNGWYRGHYSRYQDGYMAE 470
 DB 122 HNGKQFTLLDRDHDVYTGNCAYQKGGWYVYACAHSNLNGWYRGHYSRYQDGYMAE 181
 QY 471 PRGGSYSLKVVMMIRP 487
 DB 182 YRGGSYSLKVVMMIRP 198

RESULT 12
 Q98U9 PRELIMINARY; PRT; 197 AA.

ID Q98U9; AC Q98U9; DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Fibrinogen-like protein (fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amano T., Yoshizato K.;
 RT "Isolation of genes involved in intestinal remodeling during anuran
 metamorphosis.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF170323; AAK1499.1; -.
DR HSSP; P02671; 1PZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
FT NON_TER 1
FT NON_TER 197
SQ SEQUENCE 197 AA; 22954 MW; 3409C6314E853896 CRC64;

Query Match 33.7%; Score 906.5; DB 13; Length 197;
Best Local Similarity 84.9%; Pred. No. 9,6e-56;
Matches 163; Conservative 11; Mismatches 15; Indels 3; Gaps 2;

QY 198 AOLEEHQRPV--SARVPQPPPAAPPRVYQPTNRIINOISTNEIOSDONLKVLPPL 255
DB 1 SLEBCHKRPVPTQKPLPQ--PPQPNKYVNPENNRINIOISTNEIOGDONLKVLPPL 59
QY 256 PTMPLTSLPSSTDKSPGWRDCLQLEDGHTSIVYKPEPTNRLMQWCDQRPDGG 315
DB 60 PTMPLTNSNSTDXPSGPMKDCLOAMEGHTSIVYKPEPTNRLMQWCDQRPDGG 119
QY 316 WTIVQRRLDGSVNFPRNMETYKQGFNIDGEYWLGLENIYWLITNOGNKLLVTMEDWSGR 375
DB 120 WTIVQRRLDGSVNFPRNMETYKLGFGNHGEYWLGLENIYWLITNOGNKLLITMEDWSGR 179
QY 376 KYFAFYASFRLE 387
DB 180 KMFAFYASFRLE 191

RESULT 13

Q8C219 PRELIMINARY; PRT; 513 AA.
ID 090219
AC 090219;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Angiopoietin-1.
GN ANGPT1 OR ANG1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21391693; PubMed=11500985;
RA Pham V.N., Roman B.L., Weinstein B.M.;
RT "Isolation and expression analysis of three zebrafish angiopoietin genes.";
RT Dev. Dyn. 221:470-474 (2001).
RU EMBL; AF379602; AAK83347.1; -.
DR ZFIN; ZDB-GENE-010817-1; angpt1.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
SQ SEQUENCE 513 AA; 58360 MW; 0627777AA39847D8B CRC64;

Query Match 21.9%; Score 588.5; DB 13; Length 513;
Best Local Similarity 30.5%; Pred. No. 6,2e-33;
Matches 163; Conservative 87; Mismatches 200; Indels 85; Gaps 19;

QY 9 WVLGF-LIAMGAVV---GOEDFEGTEEGSPREFIYLN-----RYKRAESQDKCTYTFI 59
DB 2 WVGCFIALLIVVACGGVEQKTDGWSTPKS-----HSSGRRTYHRIOHQ--CSYTFI 55
QY 60 VPOQRTGATCVNSKEPEVLENNRYHQ---ELLENNELIKQROIEFTLQO-LVKYDG 114
DB 56 LDES--DGNTCREFFSGTAYNANALQRPAPDEALSNQKIQOLHEVWENYTWOLKLEN 113
QY 115 GIVSEYKL-----LRKSRMNSRVLTQVQLLHEI-----IR 147

DB 114 YIKDNKTEWVQIQGSAVHNHTAMLEMGTSLSIQTABQTRKITDVEYVQLNQTSLRIQ 173
QY 148 KRDNALELSQENRININQTAQMLQASKYKDELEHKYCHLATLANOSEIILAQLEHCQRPV 207
DB 174 LLENSLSTNLEKQMIQINIKIHDKNGFLEEKQOELE-----DRRQEL 220
QY 208 PSARVPQPPPAAPPRVYQPTNRIINOISTNEIOSDONLKVLPPLPPLTSL--- 264
DB 221 ESIRTEKSDIQALVSR--QSSVIRELENQLSRATGNSTALQROQODLMSRSLSLCAK 278
QY 265 -----PSSTDK--DSGWRDCLQLEDGHTSIVYKPEPTNRLMQWCDQRPD 313
DB 279 DATAVEPNSTKQADEBKRRDCAQLYQAGFQNGYTTINISQETRK--YVCWESAG 335
QY 314 GGVTVIQRLDGSVNFPRNMETYKQGFNIDGEYWLGLENIYWLITNOGNKLLVTMEDWS 373
DB 336 GGVTVIQRLDGSVNFPRNMETYKLGFGNHGEYWLGLENIYWLITNOGNKLLITMEDWS 395
QY 374 GRKYFAFYASFRLEPSEYVYKLLGRYHGNAG--DSFTWNGKQFTTLBDHDVYGNCA 431
DB 396 GHOAFSQYDSFHDSEKQKRLFLKTHSGTAGQSLSAVH-GADFTKVDNDNCTCKA 454
QY 432 HYQGGWYNACASHNLNGVYRGHYRSRYQGVYMAERGGSYSLKRYVMIR 486
DB 455 LMSGGWYDACPSNLNGVYRQGHVQKF-NGIKMHYFKGSPYSLSRSTVMIR 508

RESULT 14

Q8C2K6 PRELIMINARY; PRT; 498 AA.
ID 08C2K6
AC 08C2K6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Angiopoietin.
DS Mus musculus (Mouse).
OS Mus musculus; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RU Nature 420:563-573 (2002).
DR EMBL; AK088439; BAC40354.1; -.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C.1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN AG_C DOMAIN; 1.
SQ SEQUENCE 498 AA; 57475 MW; 285D957468C5D800 CRC64;

Query Match 21.3%; Score 571.5; DB 11; Length 498;
Best Local Similarity 29.7%; Pred. No. 9,2e-32;
Matches 149; Conservative 83; Mismatches 175; Indels 95; Gaps 14;

QY 43 RYKRAESQDKCTYTFIVP-----QQVTVGATCVNSK--RP-----EVL 79
DB 32 RYNIHQGQ--CAVTFILPEHDGNCRESATQVNTNALQEDAHVEBDSQQLQHLHEV 89
QY 80 LENRVKQELINNELIK-QKROIEFTLQO-----LVKVDGIVSEYVQLRKRESRN 129
DB 90 MEN--YTWOLQKLENYIVENKSEMAIQCNNAVONHTATWLETGTSLSQGT--AEQTRK 144
QY 130 MNSRVTLQVQLLHEIRKRDNALELSQENRININQTAQMLQASKYKDELEHKY----- 163
DB 145 LTVDETQVNLQTRLEIQLLENSLSTYKLEKQLLQQTNELIKTHEKNSLLEHKILENEGK 204
QY 184 -----CHLATLANOSEIILAQLEHCQRPVAPPPAAPPVYQPTYN 231

```

Db 205 HHEEDLTKEKENIQLVSRQTFIIQLEIKQLSPA----- 240
Qy 232 RIINOISTNEISODNKLXLPPLPTMPLTSS---LPSSTDKPSGPPWRDCLQALBEDHD 287
Db 241 -----TNNNSILQKQOLEMDAVHNLVSLCTKEGVLLKGGKKEEKPPRDCADYQAGFN 295
Qy 288 TSSIVKRENTNRLMQWCDQGRHDPGGWTVIQRLLDSVNFPRWERYKQFGNIDEX 347
Db 296 KSGITITIFNNNPEPKVFCNMDVNGGWTVIQHRBDSLDLQRMKSEYKMGFGNPSGEY 355
Qy 348 WGLENIYWLITNGYKYLVTMEDWSGRKVFAYASFRLEPSEYKRLGRYHGNAG-- 405
Db 356 WIGNERIFAITSQQRQYMLRIELMDWEGNRAVSQYDRFPHGNKQNYRLYLNGHGTACKQ 415
Qy 406 DSFTWNGKQFTLLDRHDVYTGNCAYHOGGWTYNACASHNLNCGWYTRGHYSRYODG 465
Db 416 SSIILH-GADFSKTDADNDNCMKCALMLTGWMFDACGPNLNGMFTAGQNHKL-NG 473
Qy 466 VYMAEPFGSGYSLSKKVYMMIRP 487
Db 474 IKMHYFKGPSYSLRSTTMMIRP 495

```

RESULT 15

```

Q9BDY8
ID Q9BDY8 PRELIMINARY; PRT; 498 AA.
AC Q9BDY8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Angiopoietin 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2153163; PubMed=11230987;
RA Kim I., Moon S.O., Han C.Y., Pak Y.K., Moon S.K., Kim J.Y., Koh G.Y.;
RT "The angiopoietin-tie2 system in coronary artery endothelium prevents
RT oxidized low-density lipoprotein-induced apoptosis.";
RL Cardiovasc. Res. 49:872-881(2001).
DR EMBL; AF233227; AAK14992.1; -.
DR HSSP; P02671; 1FZD.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C DOMAIN; 1.
SQ SEQUENCE 498 AA; 57413 MW; A8C1C8BF656061876 CRC64;

```

Query Match

Best local similarity 21.0%; Score 565; DB 6; Length 498;
Matches 151; Conservative 92; Mismatches 195; Indels 84; Gaps 16;

```

Qy 14 LAAMGAVAGDEGFEETEGSFRFIYLNRYKRGESQDKCTYFTIYVQ-----QRYTG 67
Db 10 LAAILTHIGCSNQRSPENG-----RRYRIQHGO-CAYTFILPHEHDCNCRESTTD 60
Qy 68 ALCVNSKE---PEV-----LLENRVKQELLELNNELK-QKQIETTLQO- 108
Db 61 QYNTNALQRDAPHVQDPSQKQLCHLEHVEN--YTQMLCKIENYIENMKSEWAQIQON 118
Qy 109 -----LVKYDGVIVSEVKLRKESRNNSRVYQLYMQLLHETIRKRDVALLSOLEN 160
Db 119 AVQNHATATMLEIGTSLISQT--AEQTRKLTIDVETQVNLQTSRLQILENSLSYKLEK 175
Qy 161 RIINOTADMLQASKYKDLHENYUHLATLHANSERIQLAEHCORVPSARVPQPPAA 220
Db 176 QLLQQTNELKHEKNSLLEKHEKHELDTLKEKENIQLGLVTR----- 225
Qy 221 PPRVQPTPTNRIINOISTNE--IOSDNKLXLPPLPTMPLTSLPSSTDKPS----- 272
Db 226 --QTYIIQLELKKQLNRATNNNSVLQKQO-----LEIMDTVHNLVNLCTKEGVLLKGG 275

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```

Qy 273 -----GWRDCLQALBEDHDTSSIYVKRENTNRLMQWCDQGRHDPGGWTVIQRLLDSV 327
Db 276 KKEEVKPFPRDCADYQAGFNKSGITITIFINNPEPKVFCNMDLNGGWTVIQHRBDSL 335
Qy 328 NFRNMEITYQGFNIDGEYWLLENIYWLITNGYKYLVTMEDWSGRKVFAYASFRLE 387
Db 336 DFORMKKEYMGFGNPSGEYWLGNERTFAITSQRTTLTFLMDWEGNRAVSQYDRFHIG 395
Qy 388 PSEYKRLGRYHGNAG--DSFTWNGKQFTLLDRHDVYTGNCAYHOGGWTYNACAH 445
Db 396 NEKQNYRLYLKSGHGTAGKQSSLIH-GADFSKTDADNDNCMKCALMLTGWMFDACGP 454
Qy 446 SNLNGWYRGGHYSRYODGVYMAEPFGSGYSLSKKVYMMIRP 487
Db 455 SNLNGWYRGGHYSRYODGVYMAEPFGSGYSLSKKVYMMIRP 495

```

Search completed: July 30, 2004, 12:37:32
Job time : 46 secs

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: August 6, 2004, 12:25:23 ; Search time 860 Seconds
(without alignments)
10734.110 Million cell updates/sec

Title: US-10-018-386-1

Perfect score: 1 gaaatgagctgctgcgga.....aaaaaaaaaaaaa 2173

Sequence: 1 gaaatgagctgctgcgga.....aaaaaaaaaaaaa 2173

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124039041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_25Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002s:*
7: Geneseq2003as:*
8: Geneseq2003bs:*
9: Geneseq2003cs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2173	100.0	2173	4	AAf29738 Human ang
2	2146.2	98.8	2288	6	AA252359 NSBO gene
3	2146.2	98.8	2288	6	AA142455 Human mat
4	2134.2	98.12	2154	3	AA172856 CDNA c10n
5	2132.6	98.1	2290	2	AAx36341 Human T1E
6	2132.6	98.1	2290	4	AAc86961 Nucleotid
7	2132.6	98.1	2290	4	AA21377 Human CDN
8	2132.6	98.1	2290	6	AB65529 Human T1E
9	2132.6	98.1	2290	6	AA21377 Human T1E
10	2132.6	98.1	2290	7	AA21377 Human T1E
11	2132.6	98.1	2290	7	AA21377 Human T1E
12	2132.6	98.1	2290	7	AA21377 Human T1E
13	2132.6	98.1	2290	7	AA21377 Human T1E
14	2132.6	98.1	2290	7	AA21377 Human T1E
15	2132.6	98.1	2290	7	AA21377 Human T1E
16	2132.6	98.1	2290	7	AA21377 Human T1E
17	2132.6	98.1	2290	7	AA21377 Human T1E
18	2132.6	98.1	2290	7	AA21377 Human T1E
19	2132.6	98.1	2290	7	AA21377 Human T1E
20	2132.6	98.1	2290	7	AA21377 Human T1E
21	2132.6	98.1	2290	7	AA21377 Human T1E
22	2132.6	98.1	2290	7	AA21377 Human T1E
23	2132.6	98.1	2290	7	AA21377 Human T1E

24	2132.6	98.1	2290	8	ADA61490 Homo sapi
25	2132.6	98.1	2290	8	ADB19275 Novel hum
26	2132.6	98.1	2290	8	ADB27816 CDNA enco
27	2132.6	98.1	2290	8	ADA66295 Novel hum
28	2132.6	98.1	2290	8	ADB15859 Human PRO
29	2132.6	98.1	2290	8	ADA47645 Human PRO
30	2132.6	98.1	2290	8	ADA67440 Human PRO
31	2132.6	98.1	2290	8	ADB30447 CDNA enco
32	2132.6	98.1	2290	8	ADA85743 Novel hum
33	2132.6	98.1	2290	8	ADA69555 Human PRO
34	2132.6	98.1	2290	8	ADA79259 Human PRO
35	2132.6	98.1	2290	8	ADA87398 Novel hum
36	2132.6	98.1	2290	8	ADA16600 Human PRO
37	2132.6	98.1	2290	8	ADA91692 Novel hum
38	2132.6	98.1	2290	8	ADA14755 Human PRO
39	2132.6	98.1	2290	8	ADA47327 Human sec
40	2132.6	98.1	2290	8	ADB18716 Novel hum
41	2132.6	98.1	2290	8	ADA93931 Human PRO
42	2132.6	98.1	2290	8	ADB19827 Novel hum
43	2132.6	98.1	2290	8	ADB31319 Human PRO
44	2132.6	98.1	2290	8	ACD98557 Novel hum
45	2132.6	98.1	2290	8	ADA74393 Human PRO

ALIGNMENTS

RESULT 1	AAf29738	standard; CDNA; 2173 BP.
XX	AAf29738;	
XX	05-APR-2001	(first entry)
DE	Human angiotensin-7 (ANG-7) coding sequence.	
XX	Human; angiotensin-7; ANG-7; angiotensin; cancer; wound healing;	
KW	diabetic retinopathy; macular degeneration; cardiovascular disease;	
KW	reproductive system; ss.	
OS	Homo sapiens.	
XX	MO200102434-A1.	
PD	11-JAN-2001.	
PF	30-JUN-2000; 2000WO-US018170.	
XX	02-JUL-1999; 99EP-00113502.	
XX	(FARB) BAYER AG.	
PA	Friedrich G, Hagen G, Wick M, Zubov D, Dubois-Stringfellow N;	
PI	WPI; 2001-123103/13.	
DR	P-PSDB; AAB66340.	
XX	Inhibiting angiotensin for treating cancer, wound healing, diabetic	
PT	retinopathies, macular degeneration, cardiovascular diseases, by	
PT	administering angiotensin-7 polypeptide or its fragments.	
PS	Claim 13; Fig 1; 86pp; English.	
XX	The present invention describes a method of preventing angiogenesis by	
XX	administering angiotensin-7 (ANG-7) nucleic acid, protein, fragment or	
XX	derivative. This can be used in the treatment of angiogenesis-related	
XX	diseases, including cancer, wound healing, macular degeneration,	
XX	cardiovascular diseases, diabetic retinopathies, infections and	
XX	conditions of the reproductive system such as regulation of placental	
XX	vascularization, and also may be used as an abortifacient. Note: In the	
XX	specification, ANG-7 is also referred to as being angiotensin-7	

Sequence 2173 BP, 538 A, 659 C, 611 G, 365 T, 0 U, 0 Other;
Query Match 100.0%; Score 2173; DB 4; Length 2173;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAATGAGGCTGCTGCGAGCGGCTGAGAGATGAACCCCAAGCCCTGAGCCTGCGGAGCG 60
DB 1 GAAAATGAGGCTGCTGCGAGCGGCTGAGAGATGAACCCCAAGCCCTGAGCCTGCGGAGCG 60
QY 61 TGGCACTGAGAGCGGCTGAGAGCTACTGTGAGGGAAGAAAGTTGTGAGCAGCGCCGCA 120
DB 61 TGGCACTGAGAGCGGCTGAGAGCTACTGTGAGGGAAGAAAGTTGTGAGCAGCGCCGCA 120
QY 121 GGAACCTTGGCCAGCCCTGAGCCCAAGCCTTCTGCGGAGCCTCTGTGAGAGGCAAGCCAG 180
DB 121 GGAACCTTGGCCAGCCCTGAGCCCAAGCCTCTGTGAGAGGCAAGCCAG 180
QY 181 TGGAGCCCAAGTGAAGGAGGAGGCTGTGAGAGCAGCGGCTGCAACTGAGAAACCCCTCC 240
DB 181 TGGAGCCCAAGTGAAGGAGGAGGCTGTGAGAGCAGCGGCTGCAACTGAGAAACCCCTCC 240
QY 241 AGAGGCCATGAGCAGGCTGCCCGCTGAGCGGCAGAGGTGAAGCATGTGAGAGCCGCC 300
DB 241 AGAGGCCATGAGCAGGCTGCCCGCTGAGCGGCAGAGGTGAAGCATGTGAGAGCCGCC 300
QY 301 GGAAGCCAGCAGAGGGAAGAGGCTTTTCAATATTTTCAATAAGAAATTAACCACTT 360
DB 301 GGAAGCCAGCAGAGGGAAGAGGCTTTTCAATATTTTCAATAAGAAATTAACCACTT 360
QY 361 TTGCAAAAGACATGAGAGGCACGTGCTGACATGCTGTGAGCTCGAGATGCTGCTGCA 420
DB 361 TTGCAAAAGACATGAGAGGCACGTGCTGACATGCTGTGAGCTCGAGATGCTGCTGCA 420
QY 421 TGGAGAGCTTTGAGAGGCCAGAGAGCGTTTGAAGGGCACTGAGAGAGGCTTCGCAAGAG 480
DB 421 TGGAGAGCTTTGAGAGGCCAGAGAGCGTTTGAAGGGCACTGAGAGAGGCTTCGCAAGAG 480
QY 481 AGTTCATTAACTTAACAGAGTACAAAGCGGAGCGGAGCTCCAGAGCAAGTGCACCTCA 540
DB 481 AGTTCATTAACTTAACAGAGTACAAAGCGGAGCGGAGCTCCAGAGCAAGTGCACCTCA 540
QY 541 CCTTCATTGTGCCCCAGCAGCGGCTCAGCGGCTGCCATCTGCTCAACTCCAAAGAGCCTG 600
DB 541 CCTTCATTGTGCCCCAGCAGCGGCTCAGCGGCTGCCATCTGCTCAACTCCAAAGAGCCTG 600
QY 601 AGGTGCTTCTGAGAAACCGAGTGCATAAGCAGAGACTAGAGCTGCTCAACATGAGCTGC 660
DB 601 AGGTGCTTCTGAGAAACCGAGTGCATAAGCAGAGACTAGAGCTGCTCAACATGAGCTGC 660
QY 661 TCAAGCAGAAAGCGGAGATCGAGCGCTGCAGCACTGTGAGAGGTGAGCGCGCATTTG 720
DB 661 TCAAGCAGAAAGCGGAGATCGAGCGCTGCAGCACTGTGAGAGGTGAGCGCGCATTTG 720
QY 721 TGAAGCAGGTGAAGCTGCTGCCAGAGAGAGCCGCAATGAACTCGCGGCTCAGCGCAGC 780
DB 721 TGAAGCAGGTGAAGCTGCTGCCAGAGAGAGCCGCAATGAACTCGCGGCTCAGCGCAGC 780
QY 781 TTTACATGAGCTCTGCAAGAGATCATTCGGAACCGGAGCAACCGCTTGAAGCTCTCC 840
DB 781 TTTACATGAGCTCTGCAAGAGATCATTCGGAACCGGAGCAACCGCTTGAAGCTCTCC 840
QY 841 AGCTGAGAAAGATCTTGAACCAAGACAGACCGGACATCTGAGCTGCGCAGCAATCA 900
DB 841 AGCTGAGAAAGATCTTGAACCAAGACAGACCGGACATCTGAGCTGCGCAGCAATCA 900
QY 901 AGGACCTGAGAGCAAGTACAGACAGCTGGCCAGCATGAGCCCAACCAATCAAGATCA 960
DB 901 AGGACCTGAGAGCAAGTACAGACAGCTGGCCAGCATGAGCCCAACCAATCAAGATCA 960
QY 961 TCGCAGAGCTTGAAGAGCACTGCGCAGAGAGTCCCTCGGCAAGCCGCTCCCGCAGCAC 1020
DB 961 TCGCAGAGCTTGAAGAGCACTGCGCAGAGAGTCCCTCGGCAAGCCGCTCCCGCAGCAC 1020

QY 1021 CCCCCTGCTGCCGCCCGGCTTACCAACCAACCCTTACCAACCGCATCATCAACCAAG 1080
DB 1021 CCCCCTGCTGCCGCCCGGCTTACCAACCAACCCTTACCAACCGCATCATCAACCAAG 1080
QY 1081 TCTCTACCAAGAGATCCAGATGACAGACCAAGCTGAAAGGTGCGGACCCCTCTGCGCA 1140
DB 1081 TCTCTACCAAGAGATCCAGATGACAGACCAAGCTGAAAGGTGCGGACCCCTCTGCGCA 1140
QY 1141 CTATGCCACTCTTACAGAGCTTCCATCTTCCACCAAGACCGTGGGCGCAATGAGAG 1200
DB 1141 CTATGCCACTCTTACAGAGCTTCCATCTTCCACCAAGACCGTGGGCGCAATGAGAG 1200
QY 1201 ACTGCTGAGAGCGCTTGAAGATGAGCCAGACAGACAGCTTCACTTCTGAGAGACCGG 1260
DB 1201 ACTGCTGAGAGCGCTTGAAGATGAGCCAGACAGACAGCTTCACTTCTGAGAGACCGG 1260
QY 1261 AGAACAACAACCGCTCATGACAGGTGTGTCAGACAGACAGACCGCGGAGCTGGA 1320
DB 1261 AGAACAACAACCGCTCATGACAGGTGTGTCAGACAGACAGACCGCGGAGCTGGA 1320
QY 1321 CCGTCACTCAGAGAGCGCTGAGATGCTCTGTTAACTTTCAAGAACTGAGAGACCTACA 1380
DB 1321 CCGTCACTCAGAGAGCGCTGAGATGCTCTGTTAACTTTCAAGAACTGAGAGACCTACA 1380
QY 1381 AGCAAGGTTTGGGAACTTGAAGGGAATTAAGCTGGGCGTGGAGACATTTACTGCG 1440
DB 1381 AGCAAGGTTTGGGAACTTGAAGGGAATTAAGCTGGGCGTGGAGACATTTACTGCG 1440
QY 1441 TGAAGAACCAAGGCAATCAAACTCTGAGTGAACATGAGAGACTGTCGCGCGCAAG 1500
DB 1441 TGAAGAACCAAGGCAATCAAACTCTGAGTGAACATGAGAGACTGTCGCGCGCAAG 1500
QY 1501 TCTTTGAGAAATACGCAAGTTTCCGCTGGAACCTGAGAGCGAGATTTAAAGCTGGCG 1560
DB 1501 TCTTTGAGAAATACGCAAGTTTCCGCTGGAACCTGAGAGCGAGATTTAAAGCTGGCG 1560
QY 1561 TGGGCGCTTACATGAGCAATGCGGCTGAGCTCTTTTCAATGAGCAACGCGCAAGCTTCA 1620
DB 1561 TGGGCGCTTACATGAGCAATGCGGCTGAGCTCTTTTCAATGAGCAACGCGCAAGCTTCA 1620
QY 1621 CCAACCTGAGAGAGATCATGATGTCTACACAGAGAACTGTGCCCTACAGAAAGGAG 1680
DB 1621 CCAACCTGAGAGAGATCATGATGTCTACACAGAGAACTGTGCCCTACAGAAAGGAG 1680
QY 1681 GCTGAGGTATTAAGCTGTGCGCACTTCCAACTCAACGAGGCTGTGATCCGCGGAGGCT 1740
DB 1681 GCTGAGGTATTAAGCTGTGCGCACTTCCAACTCAACGAGGCTGTGATCCGCGGAGGCT 1740
QY 1741 ATTACCGAGCGCTTACAGAGAGAGTCTAGGCTGAGTTCCGAGAGGCTCTTACT 1800
DB 1741 ATTACCGAGCGCTTACAGAGAGAGTCTAGGCTGAGTTCCGAGAGGCTCTTACT 1800
QY 1801 CACTCAAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
DB 1801 CACTCAAGAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CCCCCTCTGACCTCTGCTGAGCATTGCGAGAGCCCACTGATCAAGCTGAGCAAGC 1920
DB 1861 CCCCCTCTGACCTCTGCTGAGCATTGCGAGAGCCCACTGATCAAGCTGAGCAAGC 1920
QY 1921 ACAAAGAAACAATCTTCAACAGTTCACTGAGGCTGGAGAGACCGGAGTGTGATTTCT 1980
DB 1921 ACAAAGAAACAATCTTCAACAGTTCACTGAGGCTGGAGAGACCGGAGTGTGATTTCT 1980
QY 1981 GTTTTCCGAAGTCACTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
DB 1981 GTTTTCCGAAGTCACTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040
QY 2041 CTTACTTCTCTTCAACAGAGAGCCCTCATGCTCTCAAGACAGAGACAGAGACTACAGAC 2100
DB 2041 CTTACTTCTCTTCAACAGAGAGCCCTCATGCTCTCAAGACAGAGACAGAGACTACAGAC 2100

OY		2101	AACTCTTCTTTAATAATTAAGCTCTACATTAAAAACAACACTGCAAGGTAAAAAAA	2160
Db		2101	AACCTTCTCTTTAAATAATTAGCTCTACATTAAAAACAACACTGCAAGGTAAAAAAA	2160
OY		2161	AAAAAAAAAAAAAA 2173	
Db		2161	AAAAAAAAAAAAAA 2173	
RESULT 2				
ID	AAZ52359	standard; cDNA; 2288 BP.		
XX	AAZ52359			
XX	AAZ52359;			
DT	24-JUL-2000	(first entry)		
XX				
DE	NSEQ gene-11 associated with matrix remodelling.			
XX				
KW	NSEQ gene; matrix-remodeling gene; Incyte clone 2268890; Cancer;			
KM	matrix-remodeling disease; cardiomyopathy; arthritis; angiogenesis;			
KM	diabetic necrosis; atherosclerosis; fibrosis; ulceration; cytostatic;			
KM	cardioactive; antiarthritic; angiogenic; antiarteriosclerotic; antiulcer;			
ss.				
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	442..1923		
FT		/tag= a		
FT	sig_peptide	/product= "PSEO protein"		
FT		442..507		
FT		/tag= b		
PN	WO200021986-A2.			
PD	20-APR-2000.			
PE	06-OCT-1999;	99MO-US023315.		
PR	09-OCT-1998;	98US-00169289.		
PA	(INCYTE) INCYTE PHARM INC.			
PI	Walker MG, Volkmutch W, Klingler TM;			
DR	WPI; 2000-317934/27.			
DR	P-PEDB; AAY70745.			
PT	Protein co-expressed with matrix-remodeling proteins, useful in the			
PT	diagnosis and treatment of cancer, cardiomyopathy, arthritis, and			
PT	angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and			
PT	ulceration.			
PS	Claim 1; Page 44-45; 5pp; English.			
XX				
CC	The present sequence is NSEQ gene that is co-expressed with one or more			
CC	known matrix-remodeling genes in a number of biological samples using an			
CC	expression vector. This sequence was identified from the Incyte clone			
CC	2268890. The gene, protein, and antibody sequences can be used in the			
CC	diagnosis, and treatment or prevention of a disease associated with its			
CC	altered expression. The diseases that can be treated are matrix-			
CC	remodeling diseases, including cancer, cardiomyopathy, arthritis,			
CC	angiogenesis, diabetic necrosis, atherosclerosis, fibrosis, and			
CC	ulceration			
XX				
SQ	Sequence 2288 BP; 548 A; 689 C; 647 G; 404 T; 0 U; 0 Other;			
Query Match	98.8%; Score 2146.2; DB 3; Length 2288;			
Best Local Similarity	99.4%; Pred. No. 0;			
Matches 2154; Conservative	0; Mismatches 13; Indels 0; Gaps 0			

Db	73	AAATGAGGCTGCTGTCGGACGAGCTGGAATGGAATCCCAAGCCCTGGACCTTGCCAGGCTG	132
Qy	63	GCAC TGAGGCAAGCGGCTGACGCTCACTGTGAGGGGAAACAAGGTTGTGACGAGCCCGCAGG	122
Db	133	GCAC TGAGGCAAGCGGCTGACGCTCACTGTGAGGGGAAACAAGGTTGTGACGAGCCCGCAGG	192
Qy	123	ACCCTTGACCAAGCCCTGAGCCCAAGCCTCTGCGGAGGCGCTTGTGAGGCGAGACCAATG	182
Db	193	ACCCTTGACCAAGCCCTGAGCCCAAGCCTCTGCGGAGGCGCTTGTGAGGCGAGACCAATG	252
Qy	183	GAGCCCAATGAGGCGAGGCTGCTTGGACCAACCCGCTCGAATCTCAGGAACCCCTCCAG	242
Db	253	GAGCCCAATGAGGCGAGGCTGCTTGGACCAACCCGCTCGAATCTCAGGAACCCCTCCAG	312
Qy	243	AGGCAATGAGCAAGGCTGCGCCGCTGACGAGCCAGGGTGAAGCATGTGAGGAGCCGCGG	302
Db	313	AGGCAATGAGCAAGGCTGCGCCGCTGACGAGCCAGGGTGAAGCATGTGAGGAGCCGCGG	372
Qy	303	AGCCAGCAAGAGGGAAGAGGCTTCAATGATTTCAATTCACAAAGATTAACCAACATTTT	362
Db	373	AGCCAGCAAGAGGGAAGAGGCTTCAATGATTTCAATTCACAAAGATTAACCAACATTTT	432
Qy	363	GCAAAAGCAATGAGGCGCACTGTGGGTACATGCTGTGGGTGGCTCGGACCTGAGCCATG	422
Db	433	GCAAAAGCAATGAGGCGCACTGTGGGTACATGCTGTGGGTGGCTCGGACCTGAGCCATG	492
Qy	423	GGAAGCTGTGAGGCGCAGAGGAGCGGTTTGTAGGGCACTGAGAGGGCTGCGCAAGAG	482
Db	493	GGAAGCTGTGAGGCGCAGAGGAGCGGTTTGTAGGGCACTGAGAGGGCTGCGCAAGAG	552
Qy	483	TTCAATTAACCTAAACAAGTAAACCGGGCGGGCGAATCCCGAGCAATGACCTACAC	542
Db	553	TTCAATTAACCTAAACAAGTAAACCGGGCGGGCGAATCCCGAGCAATGACCTACAC	612
Qy	543	TTCAATTGGCCCAAGCGGGGTACCGGGTCCACTCTGCAATCCCAAGAGGCTTGAG	602
Db	613	TTCAATTGGCCCAAGCGGGGTACCGGGTCCACTCTGCAATCCCAAGAGGCTTGAG	672
Qy	603	GTGCTTTGAGGAACCGATGTCATTAAGCAGGACTAGAGCTGCTCAACAATGAGGCTGCTC	662
Db	673	GTGCTTTGAGGAACCGATGTCATTAAGCAGGACTAGAGCTGCTCAACAATGAGGCTGCTC	732
Qy	663	AAGCAAGAGCGCGAGATGAGACGCTGACAGACTGGTGAAGGTGAGCGCGGCAATTGTG	722
Db	733	AAGCAAGAGCGCGAGATGAGACGCTGACAGACTGGTGAAGGTGAGCGCGGCAATTGTG	792
Qy	723	AGCGAGTGAAGCTGCTGCGCAAGAGAGGCGCAACATGAATCTGCGGGGTCAACGACCTC	782
Db	793	AGCGAGTGAAGCTGCTGCGCAAGAGAGGCGCAACATGAATCTGCGGGGTCAACGACCTC	852
Qy	783	TACATGCAAGCTCTGCAACGATATATCCGAAGGGGCAACCGCTTGAAGCTCTCCAG	842
Db	853	TACATGCAAGCTCTGCAACGATATATCCGAAGGGGCAACCGCTTGAAGCTCTCTCCAG	912
Qy	843	CTGAGGAACAGGATCTTGAAACAAGACAGCCGACATGCTGACGCTTGCCAGCAAGTACAAG	902
Db	913	CTGAGGAACAGGATCTTGAAACAAGACAGCCGACATGCTGACGCTTGCCAGCAAGTACAAG	972
Qy	903	GACCTGGAAGCAAGTAAACACCACTTGCCCAACTGCGCCCAACCAATCGAAGATCAATC	962
Db	973	GACCTGGAAGCAAGTAAACACCACTTGCCCAACTGCGCCCAACCAATCGAAGATCAATC	1032
Qy	963	GCGCAGCTTGAAGAGCACTGCAAGAGGCTGCTGAGCAGGCGCGTCCCGCAGCAACC	1022
Db	1033	GCGCAGCTTGAAGAGCACTGCAAGAGGCTGCTGAGCAGGCGCGTCCCGCAGCAACC	1092
Qy	1023	CCCGCTGCCCCCGGCTCTAACCAACCACTTAACACCGATCATCAACCAAGTAC	1082
Db	1093	CCCGCTGCCCCCGGCTCTAACCAACCACTTAACACCGATCATCAACCAAGTAC	1152
Qy	1083	CTTACCAACGAGATCAAGATGACAGAACTGAAGAGTGTGACACCCCTCTGCCACT	1142


```

Db      1153 TCTACCAACGAGATCCAGAGTGAACGAACTGAAAGTGTGCCACCCCTCTGTCCACT 1212
QY      1143 ATGCCCACTCTCACAGAGCTCCCATCTTCCACCGAACGCCCTGGGCCCCTATGAGAGAC 1202
Db      1213 ATGCCCACTCTCACAGAGCTCCCATCTTCCACCGAACGCCCTGGGCCCCTATGAGAGAC 1272
QY      1203 TGGCTGAGAGCCCTGAGAGATGGCCACGACCAAGCTTCATCTACTGTGTAAGCCGAG 1262
Db      1273 TGGCTGAGAGCCCTGAGAGATGGCCACGACCAAGCTTCATCTACTGTGTAAGCCGAG 1332
QY      1263 AACACCAACCGCTCTATGAGAGTGTGTGCGACGACGACGACCCCGGGGCTGAGAC 1322
Db      1333 AACACCAACCGCTCTATGAGAGTGTGTGCGACGACGACGACCCCGGGGCTGAGAC 1392
QY      1323 GTTCATCAAGAGAGCGCTGATGAGCTGTGTTAACTTCTTCAGAACTGGAGAGCTGAC 1382
Db      1393 GTTCATCAAGAGAGCGCTGATGAGCTGTGTTAACTTCTTCAGAACTGGAGAGAGCTG 1452
QY      1383 CAAGGGTTTGGGAACTTGAACGGCGAATCTGAGCTGGGCTGGAGAACTTATCTGGGCTG 1442
Db      1453 CAAGGGTTTGGGAACTTGAACGGCGAATCTGAGCTGGGCTGGAGAACTTATCTGGGCTG 1512
QY      1443 ACGAACCAAGGCACTACAACTCTGTGTGACCATGAGAGAGTGTGCGCGCAAAAGTC 1502
Db      1513 ACGAACCAAGGCACTACAACTCTGTGTGACCATGAGAGAGTGTGCGCGCGCAAAAGTC 1572
QY      1503 TTTTGCAATATAGCCAGTTTCCGCTTGGAACTTGAGAGAGATATTATAGTGTGGCTG 1562
Db      1573 TTTTGCAATATAGCCAGTTTCCGCTTGGAACTTGAGAGAGATATTATAGTGTGGCTG 1632
QY      1563 GGGCGCTACATGAGCATGCGGGTACTCTTTAATGACCAACGCGAAGAGAGTTCACC 1622
Db      1633 GGGCGCTACATGAGCATGCGGGTACTCTTTAATGACCAACGCGAAGAGTTCACC 1692
QY      1623 ACCCTGAGAGAGATCATGATGTCTACACAGGAACTGTGCCACTACCAAGAGAGAGC 1682
Db      1693 ACCCTGAGAGAGATCATGATGTCTACACAGGAACTGTGCCACTACCAAGAGAGAGC 1752
QY      1683 TGGTGTATTAACGCTGTGCTCCACTCCAACTCAACGCGGGTGTGTACCGGGGGGGCAT 1742
Db      1753 TGGTGTATTAACGCTGTGCTCCACTCCAACTCAACGCGGGTGTGTACCGGGGGGGCAT 1812
QY      1743 TACCGAGCGCTTACAGAGCGAGTCTAATGAGGCTGAGTTCCGAGAGGCTCTTACTCA 1802
Db      1813 TACCGAGCGCTTACAGAGCGAGTCTAATGAGGCTGAGTTCCGAGAGGCTCTTACTCA 1872
QY      1803 CTCAGAAAGTGTGATATGATTCGAGCGGAAACCCCAACCTTCCATAGCCAGAGCTCC 1862
Db      1873 CTCAGAAAGTGTGATATGATTCGAGCGGAAACCCCAACCTTCCATAGCCAGAGCTCC 1932
QY      1863 CCCTCTGACCTCTGTGGCCATTGTCAGAGAGCCCACTGGTCACTGTCACAGAGAC 1922
Db      1933 CCCTCTGACCTCTGTGGCCATTGTCAGAGAGCCCACTGGTCACTGTCACAGAGAC 1992
QY      1923 AAAGAAACAATCTCTCAACAGTTTCAATCCCTGAGGCTGGAGAGCCGGAGATGCTGAT 1982
Db      1993 AAAGAAACAATCTCTCAACAGTTTCAATCCCTGAGGCTGGAGAGCCGGAGATGCTGAT 2052
QY      1983 TTTCCGAGTCACTGAGCGAGTGAATGAATGCAATGCAATGCAATGCAATGCAATGCA 2042
Db      2053 TTTCCGAGTCACTGAGCGAGTGAATGAATGCAATGCAATGCAATGCAATGCAATGCA 2112
QY      2043 TACTTCTCTTACACACAGAGCCCTCATGTCTTCAGAGACGAGAGAGTCAAGACAA 2102
Db      2113 TACTTCTCTTACACACAGAGCCCTCATGTCTTCAGAGACGAGAGAGTCAAGACAA 2172
QY      2103 CTCTTCTCTTAAATAAATAAGTCTTCAATTAATAAACAACAGCAAGTAAGTAAGTAAG 2162
Db      2173 CTCTTCTCTTAAATAAATAAGTCTTCAATTAATAAACAACAGCAAGTAAGTAAGTAAG 2232
QY      2163 AAAAAA 2169
Db      2233 ATATACA 2239

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RESULT 3
ID AAL42455
XX AAL42455;
XX AC AAL42455;
XX DT 11-JUL-2002 (first entry)
XX DE Human matrix-remodeling-associated nucleotide 11.
XX KW Human; ds; matrix-remodeling gene; extracellular matrix; gene;
XX KW matrix-remodeling-associated nucleotide; screening;
XX KW matrix remodeling-associated disease; angiogenesis; arthritis;
XX KW atherosclerosis; cancer; cardiomyopathy; diabetic necrosis; fibrosis;
XX KW ulceration.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 442..1923
XX FT /*tag= a
XX FT /product= "Human matrix-remodeling-associated protein 3"
XX PN US2002019000-A1.
XX PD 14-FEB-2002.
XX PF 26-MAR-2001; 2001US-00818143.
XX PR 09-OCT-1998; 98US-00169289.
XX PA (WALKER) WALKER M G.
XX PA (VOLK) VOLKMUETH W.
XX PA (KLIN) KLINGLER T M.
XX PI Walker MG, Volkmueth W, Klingler TM;
XX DR WPI: 2002-338319/37.
XX DR P-PSDB; AAO14786.
XX PT New isolated polynucleotide coexpressed with matrix-remodeling genes,
XX PT useful in diagnosis, prognosis, prevention and treatment of diseases
XX PT associated with matrix-remodeling such as angiogenesis, arthritis and
XX PT cancer.
XX PS Claim 1; Fig 3; 63pp; English.
XX CC The invention comprises human nucleotide sequences which are co-expressed
XX CC with matrix-remodeling genes. Matrix-remodeling is associated with the
XX CC construction, destruction and reorganization of extracellular matrix
XX CC components. The matrix-remodeling-associated nucleotides of the invention
XX CC are useful for screening for and purifying ligands that specifically bind
XX CC to the nucleotides of the invention. The matrix-remodeling-associated
XX CC nucleotides of the invention are also useful in the diagnosis, prognosis,
XX CC prevention, treatment and evaluation of therapies for diseases associated
XX CC with matrix remodeling (e.g. angiogenesis, arthritis, atherosclerosis,
XX CC cancer, cardiomyopathy, diabetic necrosis, fibrosis and ulceration). The
XX CC present DNA sequence represents a human matrix-remodeling-associated
XX CC nucleotide of the invention.
XX SQ Sequence 2288 BP; 548 A; 689 C; 647 G; 404 T; 0 U; 0 Other;
QY Query Match 98.8%; Score 2146.2; DB 6; Length 2288;
Db Best Local Similarity 99.4%; Pred. No. 0;
QY Matches 2154; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 3 AATGAGGCTGCTGGGAGCGGCTTGAAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 62
Db 73 AATGAGGCTGCTGGGAGCGGCTTGAAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 132
QY 63 GCACGTAGCGAGCGGCTGACGTACTGTGAGGAAAGAAAGTTGTGAGAGCGCCGACAG 122

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Db 123 GACCTGAGGACAGGCGCTGACCTGCTAGTGAGGGAAGAGGTTGAGCACCGCCCGCAGG 192
 Qy 123 ACCCTGAGCAGACCCCTGAGCCCGAGCCTCTGCGAGACCCCTCTGTGAGAGCAGAGCCAGT 182
 Db 123 ACCCTGAGCAGACCCCTGAGCCCGAGCCTCTGCGAGAGCCCTCTGTGAGAGCAGAGCAGT 252
 Qy 123 GAGCCCACTGAGAGCAGGCTGCTTGTGAGAGCCAGCCGCTGCACTCAGAGAACCCCTCCAG 242
 Db 253 GAGCCCACTGAGAGCAGGCTGCTTGTGAGAGCCAGCCGCTGCACTCAGAGAACCCCTCCAG 312
 Qy 243 AGGCGATGAGACAGGCTGCGCCGCTGACCGGCTGAGAGCTGTGAGAGCGCGCCCG 302
 Db 313 AGGCGATGAGACAGGCTGCGCCGCTGACCGGCTGAGAGCTGTGAGAGCGCGCCCG 372
 Qy 303 AGCCAGACAGAGGAGAGAGGCTTTCATAGATTCTATTCAACAGATTAACCCATT 362
 Db 373 AGCCAGACAGAGGAGAGAGGCTTTCATAGATTCTATTCAACAGATTAACCCATT 432
 Qy 363 GCAAGACCATGAGGCGCACTGTGCGTGAACATGCTGTGCTCGGACTGTGCTGCGCAG 422
 Db 423 GCAAGACCATGAGGCGCACTGTGCGTGAACATGCTGTGCTCGGACTGTGCTGCGCAG 492
 Qy 423 GAGAGCTGTGAGAGCAGAGAGAGCGCTTTTGAAGGCACTGAGAGAGGCTGCGCAAGAG 482
 Db 493 GAGAGCTGTGAGAGCAGAGAGAGCGCTTTTGAAGGCACTGAGAGAGGCTGCGCAAGAG 552
 Qy 483 TTCAATTACCTTAACAGGTAACAAGCGGCGGCGAGTCCAGAGACAGTGCATCAACC 542
 Db 553 TTCAATTACCTTAACAGGTAACAAGCGGCGGCGAGTCCAGAGACAGTGCATCAACC 612
 Qy 543 TTCAATTGAGCCCGACAGAGGAGTCAAGGAGTGCATCTGCTCAACTCCAGAGAGCTGAG 602
 Db 613 TTCAATTGAGCCCGACAGAGGAGTCAAGGAGTGCATCTGCTCAACTCCAGAGAGCTGAG 672
 Qy 603 GTGCTTCTGAGAACCCAGTGCATTAAGACAGAGCTAGAGCTGCTCAACATGAGCTGCTC 662
 Db 673 GTGCTTCTGAGAACCCAGTGCATTAAGAGCAGAGCTAGAGCTGCTCAACATGAGCTGCTC 732
 Qy 663 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 722
 Db 733 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 792
 Qy 733 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 782
 Db 793 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 852
 Qy 783 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 842
 Db 853 AAGCAGAGCGGCAATGAGAGAGCGCTGAGAGCGGAGCAACGCGTTGAGAGCTCTCCAG 912
 Qy 843 CTGAGAGACAGAGATCTGTAACAGAGAGCGGAGCATGCTGAGAGCTGCGAGAGAGTACAG 902
 Db 913 CTGAGAGACAGAGATCTGTAACAGAGAGCGGAGCATGCTGAGAGCTGCGAGAGAGTACAG 972
 Qy 903 GACCTGAGAGCAAGTACAGAGCACTGTGCGCACACTGCGCCCAACCAATTCAGAGATC 962
 Db 973 GACCTGAGAGCAAGTACAGAGCACTGTGCGCACACTGCGCCCAACCAATTCAGAGATC 1032
 Qy 963 GCGAGAGCTTGAAGAGACAGTGCAGAGAGGAGGCTGTGCGCAGAGCGGCTCCCGAGCAGC 1022
 Db 1033 GCGAGAGCTTGAAGAGACAGTGCAGAGAGGAGGCTGTGCGCAGAGCGGCTCCCGAGCAGC 1092
 Qy 1023 CCGGCTGCGCGCCCGCGGCTTACCAACCAACCACTTACCAACCGGATCATCAACAGATC 1082
 Db 1093 CCGGCTGCGCGCCCGCGGCTTACCAACCAACCACTTACCAACCGGATCATCAACAGATC 1152
 Qy 1083 TTCTACCAAGAGATTCAGAGAGTGAACAAGAGTGTGCGCAGAGCGGCTCTGCGCAGT 1142
 Db 1153 TTCTACCAAGAGATTCAGAGAGTGAACAAGAGTGTGCGCAGAGCGGCTCTGCGCAGT 1212
 Qy 1143 ATGCCACTCTACAGAGCTCCCATTTCTCAACGAGAGCGGCTCCAGAGAGC 1202

Db 1213 ATGCCACTCTACAGAGCTCCCATTTCTCAACGAGAGCGGCTCCAGAGAGC 1272
 Qy 1203 TGCTGAGAGCGCTTGAAGAGTGCAGACAGAGCTCTCACTTCACTGTGAGAGCGGAG 1262
 Db 1273 TGCTGAGAGCGCTTGAAGAGTGCAGACAGAGCTCTCACTTCACTGTGAGAGCGGAG 1332
 Qy 1263 AAGCAGAGCGGCTTGAAGAGTGCAGACAGAGCGGCTTGAAGAGCGGCTTGAAGAGCGGAG 1322
 Db 1333 AAGCAGAGCGGCTTGAAGAGTGCAGACAGAGCGGCTTGAAGAGCGGCTTGAAGAGCGGAG 1392
 Qy 1323 GTCATCAGAGAGCGCTGAGAGTGCATCTTGAAGAGTGCATCTTGAAGAGCGGAG 1382
 Db 1393 GTCATCAGAGAGCGCTGAGAGTGCATCTTGAAGAGTGCATCTTGAAGAGCGGAG 1452
 Qy 1383 CAAGGTTTGGAGACATTGAGCGGAGATCTGCTGAGAGAGATTTACTGCTG 1442
 Db 1453 CAAGGTTTGGAGACATTGAGCGGAGATCTGCTGAGAGAGATTTACTGCTG 1512
 Qy 1443 ACGAGCAGAGCACTACAAACTCTGAGTACCATGAGAGAGTGTCCGCGCAGAGT 1502
 Db 1513 ACGAGCAGAGCACTACAAACTCTGAGTACCATGAGAGAGTGTCCGCGCAGAGT 1572
 Qy 1503 TTTGCAAGATACCGCAAGTTTCCGCTTGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1562
 Db 1573 TTTGCAAGATACCGCAAGTTTCCGCTTGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1632
 Qy 1563 GGGGCTTACCATGAGCAATGAGGAGTGTCTGCTTGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1622
 Db 1633 GGGGCTTACCATGAGCAATGAGGAGTGTCTGCTTGAACCTGAGAGCGAGTATTATAAGCTGCGGCTG 1692
 Qy 1623 ACCCTGAGACAGATCATGATGTCTACACAGAGAACTGTGCGCCTTACACAGAGAGAGG 1682
 Db 1693 ACCCTGAGACAGATCATGATGTCTACACAGAGAACTGTGCGCCTTACACAGAGAGAGG 1752
 Qy 1683 TGCTGATTAACCGCTGTGCTGCTCACTCAACCTCAACCGGCTTGTGTAACCGCGGCGCAT 1742
 Db 1753 TGCTGATTAACCGCTGTGCTGCTCACTCAACCTCAACCGGCTTGTGTAACCGCGGCGCAT 1812
 Qy 1743 TACCGAGCGGCTTACAGAGAGAGTGTCTGAGGCTGAGTTCGAGAGAGGCTCTTACTCA 1802
 Db 1813 TACCGAGCGGCTTACAGAGAGAGTGTCTGAGGCTGAGTTCGAGAGAGGCTCTTACTCA 1872
 Qy 1803 CTCAAGAACTGTGATGATGATCCAGACCGAACCAGACCTTCACTTAAGCAGCTCC 1862
 Db 1873 CTCAAGAACTGTGATGATGATCCAGACCGAACCAGACCTTCACTTAAGCAGCTCC 1932
 Qy 1863 CCGTCTGAGAGCTCTGCGGAGCATTTGCGAGAGCGCAACCGTGTGAGCTGCGCAGAGC 1922
 Db 1933 CCGTCTGAGAGCTCTGCGGAGCATTTGCGAGAGCGCAACCGTGTGAGCTGCGCAGAGC 1992
 Qy 1923 AAGAGCACTCTCTCAACCACTTCACTGAGCTGAGAGAGCAGGAGTGTGATCTGT 1982
 Db 1993 AAGAGCACTCTCTCAACCACTTCACTGAGCTGAGAGAGCAGGAGTGTGATCTGT 2052
 Qy 1983 TTTCCAGAGTCACTGAGAGGAGTGAAGAACTGAATGAACTGAGTGTGTTCTGCTCC 2042
 Db 2053 TTTCCAGAGTCACTGAGAGGAGTGAAGAACTGAATGAACTGAGTGTGTTCTGCTCC 2112
 Qy 2043 TACTTCTCTCAACAGCAGAGCGGCTCATGTCTCAGAGAGAGAGAGTCAAGAGCA 2102
 Db 2113 TACTTCTCTCAACAGCAGAGCGGCTCATGTCTCAGAGAGAGAGAGTCAAGAGCA 2172
 Qy 2103 CTCTTTCTTTAATTAATTAAGTCTCAATATAAACAACACTGCAAGTAAAAA 2162
 Db 2173 CTCTTTCTTTAATTAATTAAGTCTCAATATAAACAACACTGCAAGTAAAAA 2232
 Qy 2163 AAAAAA 2169
 Db 2233 ATATACA 2239

RESULT 4
 AA17856

ID AAI72856 standard; CDNA; 2154 BP.
 AC AAI72856;
 DT 12-AUG-2002 (first entry)
 DE CDNA clone AR3, ATCC 207063.
 XX
 XX Gene: angiotensin-like protein 2; AR2; angiotensin-like protein 3; AR3;
 KM apple crisp protein; APPLE; cocoa crisp protein; COCO;
 KM signal sequence cloning; secretory leader motif; angiogenesis;
 KM wound healing; transplantation; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 358..1839
 FT /tag= a
 FT /product= "Angiotensin-like protein-3"
 XX
 PN W020005938-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 31-MAR-2000; 2000MO-US008832.
 XX
 PR 01-APR-1999; 99US-0126366P.
 PR 29-MAR-2000; 2000US-00538361.
 XX
 PA (GENE) GENETICS INST INC.
 PI Racie-Collins LA, Lavallie ER;
 XX
 DR WPI; 2000-664990/64.
 DR F-PSDB; AAB47997.
 XX
 XX New angiotensin-like proteins 2 and 3, apple crisp and cocoa crisp
 PT proteins and polynucleotides, useful in treating e.g. autoimmune
 PT diseases, cancer, or central and peripheral nervous system disorders and
 PT neuropathies.
 XX
 PS Claim 24; Page 70-71; 84pp; English.
 XX
 CC The sequences given in AAI72855-58 encode angiotensin-like protein 2
 CC (AR2), angiotensin-like 3 protein (AR3), apple crisp protein (APPLE), or
 CC cocoa crisp protein (COCO), respectively. These sequences were isolated
 CC by indirect cloning techniques, e.g. signal sequence cloning, which
 CC isolates DNA based on the presence of well known secretory leader motifs.
 CC AR2 and AR3 promote angiogenesis and may therefore be used in wound
 CC healing and transplantation
 CC
 SQ Sequence 2154 BP; 528 A; 657 C; 607 G; 362 T; 0 U; 0 Other;

Query Match 98.2%; Score 2134.2; DB 3; Length 2154;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2136; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 30 GATGAACCCCAAGCCCTGAGCTGCGAGCGTGGCACTGAGGCGAGCTGAGCTACTG 89
 DB 16 GATGACCCCAAGCCCTGAGCTGCGAGCGTGGCACTGAGGCGAGCTGAGCTACTG 75
 QY 90 TAGGGAAAGAGTTGTGAGCAGCCCGCAGAGACCCCTGGCAGCCCTGGCCCCAGCTT 149
 DB 76 TAGGGAAAGAGTTGTGAGCAGCCCGCAGAGACCCCTGGCAGCCCTGGCCCCAGCTT 135
 QY 150 CTGGCGGAGCCCTGTTGAGGAGCAGAGCGAGTGGAGCCAGTGGAGGAGGAGCTTGGC 209
 DB 136 CTGGCGGAGCCCTGTTGAGGAGCAGAGCGAGTGGAGCCAGTGGAGGAGGAGCTTGGC 195
 QY 210 AGCCACCGGCTGCACTCAGGAACCCCTCCAGAGGCCATGAGACAGGCTGCCCGCTGAC 269
 DB 196 AGCCACCGGCTGCACTCAGGAACCCCTCCAGAGGCCATGAGACAGGCTGCCCGCTGAC 255

QY 270 GGCACAGGCTGAGACATGTAGAGAGCCGCCCGAGCCCAAGCTAGAGGAGAGGCTTTCA 329
 DB 256 GGCACAGGCTGAGACATGTAGAGAGCCGCCCGAGCCCAAGCTAGAGGAGAGGCTTTCA 315
 QY 330 TAGATTCTATTCAACAAGATATACACCAATTTTGGCAAGACCATGAGGCCACTGTGCGTG 389
 DB 316 TAGATTCTATTCAACAAGATATACACCAATTTTGGCAAGACCATGAGGCCACTGTGCGTG 375
 QY 390 ACATGCTGTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 449
 DB 376 ACATGCTGTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 435
 QY 450 TTTGAGGAGCACTGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 509
 DB 436 TTTGAGGAGCACTGAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
 QY 510 GCGGCGAGTCCCAAGAGCAAGTGCACCTTACCTTATTTGCTGCTGCTGCTGCTGCTGCTG 569
 DB 496 GCGGCGAGTCCCAAGAGCAAGTGCACCTTACCTTATTTGCTGCTGCTGCTGCTGCTGCTG 555
 QY 570 GTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
 DB 556 GTGTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
 QY 630 CAGAGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 689
 DB 616 CAGAGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
 QY 690 CAGAGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 749
 DB 676 CAGAGCTAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 735
 QY 750 AGCCGAGCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 809
 DB 736 AGCCGAGCACTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
 QY 810 CGCAGCGGAGCAACCGCTTGAAGCTCTCCAGCTGAGAGCAAGATCTTGAACAGACA 869
 DB 796 CGCAGCGGAGCAACCGCTTGAAGCTCTCCAGCTGAGAGCAAGATCTTGAACAGACA 855
 QY 870 GCGGACATGCTGAGAGTGGCGAGCAAGTAAAGAGCTGAGAGCAAGTAAAGAGCAAGTAA 929
 DB 856 GCGGACATGCTGAGAGTGGCGAGCAAGTAAAGAGCTGAGAGCAAGTAAAGAGCAAGTAA 915
 QY 930 GCCACACTGCGCCCAACCAACATGAGATCATGCGCAGCTTGAAGAGCACTGCCAGAG 989
 DB 916 GCCACACTGCGCCCAACCAACATGAGATCATGCGCAGCTTGAAGAGCACTGCCAGAG 975
 QY 990 GTGCTCTGCGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1049
 DB 976 GTGCTCTGCGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
 QY 1050 CCACCACTTACCAACGAGATCTTACCAACGAGATCTTACCAACGAGATCTTACCAACGAG 1109
 DB 1036 CCACCACTTACCAACGAGATCTTACCAACGAGATCTTACCAACGAGATCTTACCAACGAG 1095
 QY 1110 AACCTGAAAGTGTGCAACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1169
 DB 1096 AACCTGAAAGTGTGCAACCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1155
 QY 1170 TCCACCGAACAAGCGCGGAGCCATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1229
 DB 1156 TCCACCGAACAAGCGCGGAGCCATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1215
 QY 1230 GACACAGCTCATCTTACCTGTTGAGAGCGGAGAACCAACCGCTCTATGAGAGTGTG 1289
 DB 1216 GACACAGCTCATCTTACCTGTTGAGAGCGGAGAACCAACCGCTCTATGAGAGTGTG 1275
 QY 1290 TGGAGACAGAGAGACAGACCCCGGAGGCTGAGACCTGATATCCAGAGAGCGCTGAGTGT 1349
 DB 1276 TGGAGACAGAGAGACAGACCCCGGAGGCTGAGACCTGATATCCAGAGAGCGCTGAGTGT 1335
 QY 1350 GTTAACCTTCTTCAAGAACTGGAGAGATCAAGCAAGAGGTTTGGAGAACTTGAACGAGAA 1409

Db	1336	GTTAACCTCTTCAGGAACCTGGGAGACGTAACAAGCAAGGTTTGGAACATTGACGGCGAA	1395
QY	1410	TACTGGCTGGGCTCGGAGAACATTTACTGSGTGAAGAACCAAGGCAATCAACAACTCCTG	1469
Db	1396	TACTGGCTGGGCTCGGAGAACATTTACTGSGTGAAGAACCAAGGCAATCAACAACTCCTG	1455
QY	1470	GTGACCATGAGAGAGACTGCTCCGGGCGGCAAACTCTTTGAGAAATGCGCAGTTCCGCTG	1529
Db	1456	GTACACATGAGAGAGACTGCTCCGGCGGCAAACTCTTTGAGAAATGCGCAGTTCCGCTG	1515
QY	1530	GAACCTGAGAGCAGATATTATAGCTGCGGCTGGGCGCTACCATGCAATGCGGAGTGAC	1589
Db	1516	GAACCTGAGAGCAGATATTATAGCTGCGGCTGGGCGCTACCATGCAATGCGGAGTGAC	1575
QY	1590	TCCCTTAAATGGCAACAGGCAAGCATTCACACCTCGGCAAGAGATCATGATGCTTAC	1649
Db	1576	TCCCTTAAATGGCAACAGGCAAGCATTCACACCTCGGCAAGAGATCATGATGCTTAC	1635
QY	1650	ACAGAAACTGTGCTCACTACCAAGAGGAGGCTGTGTATTAACGCTGTGCCCACTCC	1709
Db	1636	ACAGAAACTGTGCTCACTACCAAGAGGAGGCTGTGTATTAACGCTGTGCCCACTCC	1695
QY	1710	AACTCTCAACGGGGTCTGGTACCGGGGGGCCATTACCGAGCCGCTACAGAGCGAGTC	1769
Db	1696	AACTCTCAACGGGGTCTGGTACCGGGGGGCCATTACCGAGCCGCTACAGAGCGAGTC	1755
QY	1770	TACTGGGCTGAGTTCGAGAGAGGCTCTTACTCATCTCAAGAAAGTGGATGATCATCCGA	1829
Db	1756	TACTGGGCTGAGTTCGAGAGAGGCTCTTACTCATCTCAAGAAAGTGGATGATCATCCGA	1815
QY	1830	CCGAACCCCAACACCTTCCACTAAAGCCAGCTCCCTCTCTGACCTCTGTGGCCATTGCC	1889
Db	1816	CCGAACCCCAACACCTTCCACTAAAGCCAGCTCCCTCTCTGACCTCTGTGGCCATTGCC	1875
QY	1890	AGGAGCCCAACCTGGTGCAGCTGGGCAACAGCAAAAGAAACAATCCACCAAGTCAATCC	1949
Db	1876	AGGAGCCCAACCTGGTGCAGCTGGGCAACAGCAAAAGAAACAATCCACCAAGTCAATCC	1935
QY	1950	TGAGGCTGGAGAGACCGGGAGTGTGATTTCTGTTTCCGAAATGCACTGCAACGGATGATG	2009
Db	1936	TGAGGCTGGAGAGACCGGGAGTGTGATTTCTGTTTCCGAAATGCACTGCAACGGATGATG	1995
QY	2010	GAATCGATCGATACGGTGTCTTCTGTCTCCCTCTCACTTCTCTTCAACCAAGCCCTCT	2069
Db	1996	GAATCGATCGATACGGTGTCTTCTGTCTCCCTCTCACTTCTCTTCAACCAAGCCCTCT	2055
QY	2070	CATGTCTCCAGAGACGACAGCATACAGCAAACTCTTCTTTAAATAATTAAGTCTCT	2129
Db	2056	CATGTCTCCAGAGACGACAGCATACAGCAAACTCTTCTTTAAATAATTAAGTCTCT	2115
QY	2130	ACATATAAAACACAACTGCCAAAGTAAAAAATAAAAA 2168	
Db	2116	ACATATAAAACACAACTGCCAAAGTAAAAAATAAAAA 2154	

RESULT 5
AAK36341
ID AAK36341 standard; DNA; 2290 BP.
XX
AC AAK36341;
XX
DT 01-JUL-1999 (first entry)
XX
DE Human TIE ligand NLI coding sequence.
XX
KW Human TIE ligand; NLI; NT4; NL5; NL6; Ig homology domain; angiogenesis;
KW EGF homology domain; receptor tyrosine kinase; vascular endothelial cell;
KW early haemopoietic cell; haemopoiesis; neovascularisation; wound healing;
KW vascular endothelial cell; growth inhibitor; apoptosis inducer; tumour cell;
KW vasculogenesis; detection; diagnosis; therapy; ss.
XX
SS Homo sapiens.

XX	WO9915653-A2.
PN	
XX	01-APR-1999.
PD	
XX	
XX	
PF	14-SEP-1998; 98WO-US019093.
XX	
PR	19-SEP-1997; 97US-00933821.
PR	29-OCT-1997; 97US-00960507.
XX	
PA	(GEETH) GENENTECH INC.
XX	
PI	Godowski PT, Gurney AL, Hillan K, Borstein D, Goddard A, Roy M,
PI	Ferrara N, Tumas D, Schwall R;
XX	
DR	WPI, 1999-263480/22.
DR	P-PSDB; AAY05396.
XX	
XX	
PT	New isolated TIE ligand homologs for, e.g. developing products for
PT	treatment of tumors.
XX	
PS	Claim 3, Fig 2, 132pp; English.

CC This sequence encodes the human tyrosine kinase containing Ig and EGF
CC homology domains (TIE) ligand of the invention, designated N1L. The TIE
CC receptors are receptor tyrosine kinases which are expressed in vascular
CC endothelial cells and early haemopoietic cells. The TIE receptors are
CC believed to be actively involved in angiogenesis, and may play a role in
CC haemopoiesis as well. The TIE ligand homologs can promote the survival
CC and/or growth and/or differentiation of TIE receptor expressing cells.
CC They can be used for promoting neovascularisation in wound healing and
CC for promoting angiogenic processes, such as for inducing collateral
CC vascularisation in an ischemic heart or limb, or for promoting bone
CC development and/or maturation and/or growth in a patient or muscle growth
CC and development. The TIE ligand homologs and antibodies can inhibit the
CC growth of endothelial cells and induce apoptosis of cells, particularly
CC tumour cells. They can inhibit vasculogenesis, particularly the
CC vascularisation of tumour cells. The antibodies can also inhibit
CC vascularisation of a cell in which a gene encoding an N1L, N1S, N1L8 or
CC N1L4 polypeptide is amplified. The products can also be used for
CC detection, diagnosis, drug screening and production of transgenic animals
CC
XX Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match	Best Local Similarity	Score	DB	Length
98.1%	99.8%	2132.6	2	2290
Matched	Conservative	Mismatches	Indels	Gaps
0	0	4	0	0

Db	511	GCAGAGACCAATGAGAGCCACTGTGTGGTGACATGCTGTGTGGCTCGGACTGTGTGGCTGCATG	570
QY	423	GGAGCTGTTGCAGGCCAGAGAGACGGTTTGAAGGCACTGAGAGAGGGCTCGCCAAAGAG	482
Db	571	GGAGCTGTGTGAGGCCAGAGAGAGCGGTTTGAAGGCACTGAGAGAGGGCTCGCCAAAGAG	630
QY	483	TTCAATTTAACCAAAACAGGTACCAAGCGGGCGGACAGTCCAGGACAATGACCTACACC	542
Db	631	TTCAATTTAACCAAAACAGGTACCAAGCGGGCGGACAGTCCAGGACAATGACCTACACC	690
QY	543	TTCAATGTGTGCCCCAGCAGCGGGGTCACGGGTGCATCTGTCAATCTCCAAAGAGCTTGAG	602
Db	691	TTCAATGTGTGCCCCAGCAGCGGGGTCACGGGTGCATCTGTGTCAATCTCCAAAGAGCTTGAG	750
QY	603	GTCGCTTCGAGGAACCCAGGTGCATTAAGAGGAGGTAGAGGCTGCATCAATAGACTGCTGC	662
Db	751	GTCGCTTCGAGGAACCCAGGTGCATTAAGAGGAGGTAGAGGCTGCATCAATAGACTGCTGC	810
QY	663	AAGCAGAAAGCCGACAGATGAGACGCTGTGCAGCGTGTGAAGGTGAACGGCGGCAATTGTG	722
Db	811	AAGCAGAAAGCCGACAGATGAGACGCTGTGCAGCGTGTGAAGGTGAACGGCGGCAATTGTG	870
QY	723	AGCGAGGTGAAGCTGTCTGCGCAAGAGAGCCGCAACATAGAACCTGGCGGTACGCCACTC	782
Db	871	AGCGAGGTGAAGCTGTCTGCGCAAGAGAGCCGCAACATAGAACCTGGCGGTACGCCACTC	930
QY	783	TACATGCACTCTCTGCACAGATATATCCGAAGCGGGAACAACGGCTTGAGCTCTCCAG	842
Db	931	TACATGCACTCTCTGCACAGATATATCCGAAGCGGGAACAACGGCTTGAGCTCTCCAG	990
QY	843	CTGGAGAACAGGATCTTGAAACCAAGCAGCCCAATGTCTGCAGCTGTGGCCAGCAATCAAG	902
Db	991	CTGGAGAACAGGATCTTGAAACCAAGCAGCCCAATGTCTGCAGCTGTGGCCAGCAATCAAG	1050
QY	903	GACCTGGAGCAAGATATCTGAACCAAGCCGCACTGTGGCCCAACCAATCAGATCATC	962
Db	1051	GACCTGGAGCAAGATATCTGAACCAAGCCGCACTGTGGCCCAACCAATCAGATCATC	1110
QY	963	GCGCAGCTTGAAGAGCACTGTCCAGAGGGTGTCCCTGTGGCCAGGCCCGTCCCGACCAACC	1022
Db	1111	GCGCAGCTTGAAGAGCACTGTCCAGAGGGTGTCCCTGTGGCCAGGCCCGTCCCGACCAACC	1170
QY	1023	CCCGCTGCCCCGCCCTCGGCTTACCAACCACTCACTCAACCCGATATCAACCAAGTCC	1082
Db	1171	CCCGCTGCCCCGCCCTCGGCTTACCAACCACTCACTCAACCCGATATCAACCAAGTCC	1230
QY	1083	TCTAACCAAGATCCAGATGACCAAGAACTGAAGGTGTGCGCAACCCCTCTGCCACT	1142
Db	1231	TCTAACCAAGATCCAGATGACCAAGAACTGAAGGTGTGCGCAACCCCTCTGCCACT	1290
QY	1143	ATGCCCACTTCAACCAAGCTTCCCATCTTTCACCAACCAACCCGTGTGGCTTGAAGAGC	1202
Db	1291	ATGCCCACTTCAACCAAGCTTCCCATCTTTCACCAACCAACCCGTGTGGCTTGAAGAGC	1350
QY	1203	TGCGTCGAGAGCCCTGAGAGATGAGCAGAGACAACAGCTCAATCTACTGTGAAGCCGAG	1262
Db	1351	TGCGTCGAGAGCCCTGAGAGATGAGCAGAGACAACAGCTCAATCTACTGTGAAGCCGAG	1410
QY	1263	AACACCAACCCGCTTCATCAGGTGTGTGTGCGAACCAAGACACGACCCCGGGGGCTGAGC	1322
Db	1411	AACACCAACCCGCTTCATCAGGTGTGTGTGCGAACCAAGACACGACCCCGGGGGCTGAGC	1470
QY	1323	GTCATCCAGAGACCGCTGTGATGTGCTCTGTTTAACTTTTCAAGAACTGGGAACGTACAG	1382
Db	1471	GTCATCCAGAGACCGCTGTGATGTGCTCTGTTTAACTTTTCAAGAACTGGGAACGTACAG	1530
QY	1383	CAAGGGTTTGGGAACATTGACGGCAAAATAGTGGCTGTGGGCTGTGGAGAACATTTACGCTG	1442
Db	1531	CAAGGGTTTGGGAACATTGACGGCAAAATAGTGGCTGTGGGCTGTGGAGAACATTTACGCTG	1590
QY	1443	ACGAACCAAGCACTAACAACTCTGTGTACATGAGAGATGTGTCTGGCCGCAAAATC	1502

Db	1591	ACGAAACCAAGCAACTACAAACTCTTGGTAGCATTGAGAGACTGGTCGCGCCGAAAGTC	1650
Qy	1503	TTTTCAGATATCGCCAGATTTCGCCCTGGAACTTGAGAGCCAGATTTTAAAGTCCGGCTG	1562
Db	1651	TTTTCAGAAATCGCCAGATTTCGCCCTGGAACTTGAGAGCCAGATTTTAAAGTCCGGCTG	1710
Qy	1553	GGGGGCTAACCAATGGCAATGCGGGGAGACTCCCTTTACATGCGACAAACGGCAGAGATTCAAC	1622
Db	1711	GGGGGCTAACCAATGGCAATGCGGGGAGACTCCCTTTACATGCGACAAACGGCAGAGATTCAAC	1770
Qy	1623	ACCTTGACAGAGATCATGATGTCTTACACAGAAAATTGTGCCACTACACGAAAGGAGGC	1682
Db	1771	ACCTTGACAGAGATCATGATGTCTTACACAGAAAATTGTGCCACTACACGAAAGGAGGC	1830
Qy	1663	TGGTGATATTAAGCGCTGTGGCCACTCCAACTCAACGAGGGCTGATACCGGGGGGCAT	1742
Db	1831	TGGTGATATTAAGCGCTGTGGCCACTCCAACTCAACGAGGGCTGATACCGGGGGGCAT	1890
Qy	1743	TACCGAGCCGCTACAGAGACGAGCTTACTGGGCTGATGTCGAGAGAGCTCTTACTCA	1802
Db	1891	TACCGAGCCGCTACAGAGACGAGCTTACTGGGCTGATGTCGAGAGAGCTCTTACTCA	1950
Qy	1803	CTCAAGAAAGTGTGATGATGATATCCGACCCGAAACCCCAACCTTCCACTAAGCAGCTCC	1862
Db	1951	CTCAAGAAAGTGTGATGATGATATCCGACCCGAAACCCCAACCTTCCACTAAGCAGCTCC	2010
Qy	1853	CCCTCTGACCTCTCGTGGCCATTGCCAGAGACCACCTGTGTGACAGCTGAGCCACAGAC	1922
Db	2011	CCCTCTGACCTCTCGTGGCCATTGCCAGAGACCACCTGTGTGACAGCTGAGCCACAGAC	2070
Qy	1923	AAAGAACCACTCTTCACCACTTTCATCTCGAGAGCTGGAGAGACCGGGAATGCTGATTCGT	1982
Db	2071	AAAGAACCACTCTTCACCACTTTCATCTCGAGAGCTGGAGAGACCGGGAATGCTGATTCGT	2130
Qy	1983	TTTCGGAAGTCACTGACAGCGGATATGGAATCGATCGATGCGTGTTCCTGTCCTCC	2042
Db	2131	TTTCGGAAGTCACTGACAGCGGATATGGAATCGATCGATGCGTGTTCCTGTCCTCC	2190
Qy	2043	TACTTTCCTTACACACAGACAGCCCTCATGTCTTCAGAGACAGACAGAGATTAAGACAA	2102
Db	2191	TACTTTCCTTACACACAGACAGCCCTCATGTCTTCAGAGACAGAGATTAAGACAA	2250
Qy	2103	CTCTTCTTTAAATTAATTAAGTCTCTCAATTAATAACA	2141
Db	2251	CTCTTCTTTAAATTAATTAAGTCTCTCAATTAATAATAA	2289
RESULT 6			
AAC86961			
ID	AAC86961 standard; cDNA; 2290 BP.		
XX	AAC86961;		
XX	20-APR-2001 (first entry)		
DE	Nucleotide sequence of human polypeptide PRO196.		
XX	Human; secreted protein, transmembrane protein; PRO196; PRO444; PRO183;		
KM	PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;		
KM	PRO1183; PRO1172; PRO1419; PRO4999; PRO1170; PRO248; PRO353; PRO1318;		
KM	PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO377; PRO1411; PRO4356;		
KM	PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;		
KM	PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;		
XX	ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	520..2001	
FT		/*tag= a	
FT	sig_peptide	520..585	
FT		/*tag= b	
XX			

MO200077037-A2.

21-DEC-2000.

22-MAY-2000; 2000MO-US014042.

15-JUN-1999; 99US-0139695P.

20-JUL-1999; 99US-0145070P.

26-JUL-1999; 99US-0145698P.

17-AUG-1999; 99US-0149395P.

01-SEP-1999; 99MO-US02011P.

08-SEP-1999; 99MO-US020594.

15-SEP-1999; 99MO-US021090.

15-SEP-1999; 99MO-US021547.

30-NOV-1999; 99MO-US028313.

01-DEC-1999; 99MO-US028301.

02-DEC-1999; 99MO-US028565.

07-DEC-1999; 99US-0169495P.

05-JAN-2000; 2000MO-US000219.

18-FEB-2000; 2000MO-US004341.

22-FEB-2000; 2000MO-US004342.

01-MAR-2000; 2000MO-US005601.

02-MAR-2000; 2000MO-US005841.

20-MAR-2000; 2000MO-US007377.

30-MAR-2000; 2000MO-US008433.

15-MAY-2000; 2000MO-US013358.

17-MAY-2000; 2000MO-US013705.

(GETH) GENENTECH INC.

Ashtenari AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godowski PJ, Gurney AJ, Kijavini IU, Mather JP, Napier WA, Pan J, Padoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI, Zhang Z;

WPI; 2001-050091/06.

P-PSDB; AAB31179.

Isolated nucleic acid molecule encoding a PRO polypeptide which is a transmembrane polypeptide is useful for gene therapy and identification of related polypeptides.

Claim 2; Fig 1; 244pp; English.

The present sequence encodes a human secreted and transmembrane polypeptide. The specification describes human polypeptides, designated PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288, PRO345, PRO3361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170, PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO531, PRO187, PRO337, PRO411, PRO435, PRO246, PRO265, PRO941, PRO10096, PRO6003, PRO6004, PRO350, PRO2630 and PRO6389. The biological activity of cells can be modulated with agents that bind to these polypeptides, resulting in the death of the cells. The polynucleotides encoding these polypeptides are useful in the recombinant production of the polypeptides, as a hybridisation probe to screen libraries to isolate homologous sequences, or to map the gene. They may also be used for analysing genetic disorders, and to produce transgenic animals which are useful for the development and screening of therapeutically useful reagents. The polynucleotides can also be used in gene therapy e.g. to replace a defective gene

Sequence 2250 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2133; Conservative 0; Mismatches 4; Indels 0; Gaps 0

3 AAATGAGCTGCTCGCAGCAGCGCTGAGAGTGAACCCCAACCCCTGAGACTGCCGACCTG 62

151 AAATGAGCTGCTCGCAGCAGCGCTGAGAGTGAACCCCAACCCCTGAGACTGCCGACCTG 210

QY	63	GCAATTGAGGAGGGGGCTGAGAGGCTACTGTGAGGGGAAAAGAAAGTTGTGTAGAGAGCCCGCAG	122
Db	211	GCATGTGAGGACGGGGCTGACGCTACTGTGTGGGAAAGAAAGTTGTGTAGAGAGCCCGCAG	270
QY	123	ACCCTTGGCCAGCCCTTGCCGCCAGCCCTCTCCCGAGCCCTCTGTGTGAGGCGAGGCCAGTG	182
Db	271	ACCCTTGGCCAGCCCTTGCCGCCAGCCCTCTCCCGAGCCCTCTGTGTGAGGCGAGGCCAGTG	330
QY	183	GAGCCCAGTGAGGCGAGGGCTGTGTGGAGGCCACCCGGCTTGCAACTAGGAACCCCTCCAG	242
Db	331	GAGCCCAGTGAGGCGAGGGCTGTGTGGAGGCCACCCGGCTTGCAACTAGGAACCCCTCCAG	390
QY	243	AGGCCAATGGAACAGGCTCCCGCTGACGGCCAGGGGTGAACATGTGAGAGAGCCGCCGG	302
Db	391	AGGCCAATGGAACAGGCTCCCGCTGACGGCCAGGGGTGAACATGTGAGAGAGCCGCCGG	450
QY	303	AGCCAGAGGAGGGGAAAGAGGCTTTCATGATTTCTATTCACAAAGATAACCATTTT	362
Db	451	AGCCAGAGGAGGGGAAAGAGGCTTTCATGATTTCTATTCACAAAGATAACCATTTT	510
QY	353	GCAAAAGCCATGAGAGCCACTGTGTGTGAACATGTGTGTGGTCCGAGCTGCTGGCTGCATG	422
Db	511	GCAAGGACCAATGAGAGCCACTGTGTGTGAACATGTGTGTGGTCCGAGCTGCTGGCTGCATG	570
QY	423	GGAGCTGTGGAGGCCAGAGAGACGGTTTGTGAGGGCACTGAGAGAGGCTCGCCAAAGAG	482
Db	571	GGAGCTGTGGAGGCCAGAGAGACGGTTTGTGAGGGCACTGAGAGAGGCTCGCCAAAGAG	630
QY	483	TTCAATTTACTTAACAGGTAAACCGGGCGGGCGCAATGCCAGAACATGTCACTTAAC	542
Db	631	TTCAATTTACTTAACAGGTAAACCGGGCGGGCGCAATGCCAGAACATGTCACTTAAC	690
QY	543	TTCAATTTGCCCCAGCAGCGGGTCAACGGGTGCATCTGCTCACTTCCAAAGAGCCCTGAG	602
Db	691	TTCAATTTGCCCCAGCAGCGGGTCAACGGGTGCATCTGCTCACTTCCAAAGAGCCCTGAG	750
QY	603	GTGCTTCTGAGAACCGAGTGCATTAAGCAGAGCTAAGCTGCTCAACATGAGCTGCTC	662
Db	751	GTGCTTCTGAGAACCGAGTGCATTAAGCAGAGCTAAGCTGCTCAACATGAGCTGCTC	810
QY	663	AAGCAAGAGCCGCAAGTGCAGACCTGTGAGAGCTGTGGTGAAGGTGAGACGGCGGCAATGTG	722
Db	811	AAGCAAGAGCCGCAAGTGCAGACCTGTGAGAGCTGTGGTGAAGGTGAGACGGCGGCAATGTG	870
QY	723	AAGCAGGTGAAGCTGTCTGCGAAGAGAGCGGCAACATGAATCTCGCGGTCAACCAAGTC	782
Db	871	AAGCAGGTGAAGCTGTCTGCGAAGAGAGCGGCAACATGAATCTCGCGGTCAACCAAGTC	930
QY	783	TAATGCAAGCTTCTGCACGAGATATATCCGCAAGGGGACAACGGGTTGAGAGCTTCCAG	842
Db	931	TAATGCAAGCTTCTGCACGAGATATATCCGCAAGGGGACAACGGGTTGAGAGCTTCCAG	990
QY	843	CTGAGAAACAGGATCTCTGAACCAAGACAGCCGACATGCTGTGAGCTGTGCGCAAGTACAG	902
Db	991	CTGAGAAACAGGATCTCTGAACCAAGACAGCCGACATGCTGTGAGCTGTGCGCAAGTACAG	1050
QY	903	GACTGTGAGACACAGTACCAAGACTCTGGCCACACTGGCCCAACCAATTCAGAGTATATC	962
Db	1051	GACTGTGAGACACAGTACCAAGACTCTGGCCACACTGGCCCAACCAATTCAGAGTATATC	1110
QY	963	GGCAGAGCTTGAGAGACATGACCCAGAGGGGTGCTGTGAGCCAGAGCCGCTCCCGACCAACC	1022
Db	1111	GGCAGAGCTTGAGAGACATGACCCAGAGGGGTGCTGTGAGCCAGAGCCGCTCCCGACCAACC	1170
QY	1023	CCCGGTGCCCCCGCCGGGTCTTACCAACCACTTCAACACCGCATTTATTAACCAATC	1082
Db	1171	CCCGGTGCCCCCGCCGGGTCTTACCAACCACTTCAACACCGCATTTATTAACCAATC	1230
QY	1083	TCACCAACAGATCCAGAGTACAGAGAACCTGAAGGTGTGTGCAACCCCTCTGCGCACT	1142
Db	1231	TCACCAACAGATCCAGAGTACAGAGAACCTGAAGGTGTGTGCAACCCCTCTGCGCACT	1290
QY	1143	ATGCCCACTGTCAAGAGCTCCCATTTCTACACGAAAGCCGTGGGGCCCATGAGAGAC	1202

Db 1291 ATGCCACTCTACCCAGCTCCCATTTTCCACGACACACCCCTGGGCCCATGAGAGAC 1350
 QY 1203 TGGCTCAGAGCCCTGAGAGATGACACACACAGCTTCATCTACCTGGTGAAGCCGAG 1262
 Db 1351 TGGCTCAGAGCCCTGAGAGATGACACACACAGCTTCATCTACCTGGTGAAGCCGAG 1410
 QY 1263 AATACCAACCGCTCTATGAGAGATGAGACACACAGCTTCATCTACCTGGTGAAGCC 1322
 Db 1411 AATACCAACCGCTCTATGAGAGATGAGACACACAGCTTCATCTACCTGGTGAAGCC 1470
 QY 1323 GTTCATCAGAGAGCGCTGATGAGCTCTGTTAACTTCTGAGAGCTGAGAGAGCTAAG 1382
 Db 1471 GTTCATCAGAGAGCGCTGATGAGCTCTGTTAACTTCTGAGAGCTGAGAGAGCTAAG 1530
 QY 1383 CAAGGTTTGGAGAACTTGAAGCGCAATCTGGCTGGGCTTGAAGAACTTTACTGGCTG 1442
 Db 1531 CAAGGTTTGGAGAACTTGAAGCGCAATCTGGCTGGGCTTGAAGAACTTTACTGGCTG 1590
 QY 1443 ACGAACCAAGGCACTACAACTCTGCTGACCATGAGAGAGCTGCTGGGCGGCAAGCTC 1502
 Db 1591 ACGAACCAAGGCACTACAACTCTGCTGACCATGAGAGAGCTGCTGGGCGGCAAGCTC 1650
 QY 1503 TTTTGCAATACGCCAGTTTCCGCTGAACTGAGAGAGATTTAATAGCTGGGCTG 1562
 Db 1651 TTTTGCAATACGCCAGTTTCCGCTGAACTGAGAGAGATTTAATAGCTGGGCTG 1710
 QY 1563 GGGCGCTACCATGAGAGAGCTGGGCTGCTTCTTACATGAGCAACGAGAGAGCTTACC 1622
 Db 1711 GGGCGCTACCATGAGAGAGCTGGGCTGCTTCTTACATGAGCAACGAGAGAGCTTACC 1770
 QY 1623 ACCCTGAGAGAGATCATGATGTCTACACAGAGAACTGTGCCACTACACAGAGAGAGC 1682
 Db 1771 ACCCTGAGAGAGATCATGATGTCTACACAGAGAACTGTGCCACTACACAGAGAGAGC 1830
 QY 1683 TGGTGGTAAAGCGCTGAGCCCACTCAACCGAGGCTGTGATACCGGGGGGCGCAT 1742
 Db 1831 TGGTGGTAAAGCGCTGAGCCCACTCAACCGAGGCTGTGATACCGGGGGGCGCAT 1890
 QY 1743 TACCGAGAGCGCTACACAGAGAGCTTACCTGAGCTGAGTCCGAGAGAGCTTTACTCA 1802
 Db 1891 TACCGAGAGCGCTACACAGAGAGCTTACCTGAGCTGAGTCCGAGAGAGCTTTACTCA 1950
 QY 1803 CTGAAGAAAGTGTATGATGATCCGACCGAACTCCCACTTCACTAAGCAGCTCC 1862
 Db 1951 CTGAAGAAAGTGTATGATGATCCGACCGAACTCCCACTTCACTAAGCAGCTCC 2010
 QY 1863 CCTCTGAGCTCTGCTGAGGCACTTGCAGAGAGCCAGCTGCTGAGCTGAGCTGAGC 1922
 Db 2011 CCTCTGAGCTCTGCTGAGGCACTTGCAGAGAGCCAGCTGCTGAGCTGAGCTGAGC 2070
 QY 1923 AAGAGAACTCTCTCAGAGAGCTTCTGAGGCTGAGAGAGAGAGAGAGCTGATGCT 1982
 Db 2071 AAGAGAACTCTCTCAGAGAGCTTCTGAGGCTGAGAGAGAGAGAGAGCTGATGCT 2130
 QY 1983 TTTCCGAGTCACTGAGAGAGCTGATGATGAGTGAATGATGATGATGATGATGATGAT 2042
 Db 2131 TTTCCGAGTCACTGAGAGAGCTGATGATGAGTGAATGATGATGATGATGATGATGAT 2190
 QY 2043 TACTTTCCTTCACTCAGAGAGAGCTTCTGAGGCTGAGAGAGAGAGAGAGCTAAGCA 2102
 Db 2191 TACTTTCCTTCACTCAGAGAGAGCTTCTGAGGCTGAGAGAGAGAGAGAGCTAAGCA 2250
 QY 2103 CTCTTCTTCTTAAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 2141
 Db 2251 CTCTTCTTCTTAAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 2289

RESULT 7
 AAS21377
 ID AAS21377 standard; cDNA, 2290 BP.
 XX
 AC AAS21377;

XX 24-OCT-2001 (first entry)
 XX
 DE Human CDNA sequence encoding for PRO196 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
 KW prostate; cervical; tumour necrosis factor- α ; TNF- α ; cartilage;
 KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
 KW A-peptide; factor VIIa; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000MO-US032678.
 XX
 PR 01-DEC-1999; 99MO-US028301.
 PR 01-DEC-1999; 99MO-US028634.
 PR 02-DEC-1999; 99MO-US028551.
 PR 02-DEC-1999; 99MO-US028564.
 PR 02-DEC-1999; 99MO-US028565.
 PR 09-DEC-1999; 99US-0170262P.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 20-DEC-1999; 99MO-US030999.
 PR 30-DEC-1999; 99MO-US031243.
 PR 30-DEC-1999; 99MO-US031274.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000277.
 PR 11-FEB-2000; 2000MO-US000376.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 03-MAR-2000; 2000MO-US005841.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 20-MAR-2000; 2000MO-US007377.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000MO-US019832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 10-NOV-2000; 2000MO-US030873.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-408281/43.
 DR P-PSDB; AAU12305.
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
 PT breast, prostate, cervical.
 XX
 PS Claim 3; Fig 267; 813pp; English.

XX AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PMNCs) or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
CC
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATATAGGCTGTGGGAGCGGCTGAGATGAAACCCAGCCCTGGACCTGCGAGGCTG 62
DB 151 AATATAGGCTGTGGGAGCGGCTGAGATGAAACCCAGCCCTGGACCTGCGAGGCTG 210
QY 63 GCACTGAGGAGCGGCTGACGCTACTGTAGGGAAGAAGTTGTAGCAGCCCGCAGG 122
DB 211 GCACGTAGGAGCGGCTGACGCTACTGTAGGGAAGAAGTTGTAGCAGCCCGCAGG 270
QY 123 ACCCTGGCCAGCCCTGGCCCGCCAGGCTCTGCGGAGCCCTCTGTGAGAGCAGAGCAGT 182
DB 271 ACCCTGGCCAGCCCTGGCCCGCCAGGCTCTGCGGAGCCCTCTGTGAGAGCAGAGCAGT 330
QY 183 GAGCCAGTGAAGGAGGCTGTGTGAGCAGCCAGCCCTGCACTCAGGAAACCCCTCCAG 242
DB 331 GAGCCAGTGAAGGAGGCTGTGTGAGCAGCCAGCCCTGCACTCAGGAAACCCCTCCAG 390
QY 243 AGGCCATGAGCAGGCTGCGGCTGAGCGCCAGGCTGAAGCATGTGAGAGCGCGCCGG 302
DB 391 AGGCCATGAGCAGGCTGCGGCTGAGCGCCAGGCTGAAGCATGTGAGAGCGCGCCGG 450
QY 303 AGCCAAAGCAGGAGGAGGAGGCTTCATGATTCATTACAAAGAAATTAACCAATTT 362
DB 451 AGCCAAAGCAGGAGGAGGAGGCTTCATGATTCATTACAAAGAAATTAACCAATTT 510
QY 363 GCAAAAGCCATGAGGCACTGTGCTGATCATCTGTGTGCTGGACTGCTGCTCCATG 422
DB 511 GCAAAAGCCATGAGGCACTGTGCTGATCATCTGTGTGCTGGACTGCTGCTCCATG 570
QY 423 GGAAGCTGTGAGGAGGAGGAGGAGGCTTTTGAAGGAGCCTGAGAGGCTCGGCAAGAG 482
DB 571 GGAAGCTGTGAGGAGGAGGAGGAGGCTTTTGAAGGAGCCTGAGAGGCTCGGCAAGAG 630
QY 483 TTCAATTACCTTAAACAGTAAACAAGCGGAGGAGTCCAGAGACAAGTGACCTTAACC 542
DB 631 TTCAATTACCTTAAACAGTAAACAAGCGGAGGAGTCCAGAGACAAGTGACCTTAACC 690
QY 543 TTCAATTGTGCCCCAGAGAGGAGTCAAGGCTGCTCACTCCAGAGAGGCTGAG 602
DB 691 TTCAATTGTGCCCCAGAGAGGAGTCAAGGCTGCTCACTCCAGAGAGGCTGAG 750
QY 603 GTGCTTCTGAGAGACGAGAGTCAAGAGAGCTGAGAGCTGCTCAACATGAGCTGCTC 662
DB 751 GTGCTTCTGAGAGACGAGAGTCAAGAGAGCTGAGAGCTGCTCAACATGAGCTGCTC 810
QY 663 AAGCAGAGCGGAGATCGAGAGCTGACAGAGCTGTGTAAGTGAACGGCGGCAATTGTG 722

DB 811 AAGCAGAGCGGAGATCGAGAGCTGACAGAGCTGTGTGAGAGTGAACGGCGGCAATTGTG 870
QY 723 AGGAGGTGAAGTGTGTGGCAAGAGAGCCGCAATGAACTCGGCGGCTCAAGAGCTC 782
DB 871 AGGAGGTGAAGTGTGTGGCAAGAGAGCCGCAATGAACTCGGCGGCTCAAGAGCTC 930
QY 783 TACATGAGCTCTGACAGAGATCATCCGAGCGGAGCAACGCTTGAAGCTCTCCAG 842
DB 931 TACATGAGCTCTGACAGAGATCATCCGAGCGGAGCAACGCTTGAAGCTCTCCAG 990
QY 843 CTGAGAGACGAGATCTGAAACCAAGACCCGACATCTGCACTGGCCAGAAATGTAAG 902
DB 991 CTGAGAGACGAGATCTGAAACCAAGACCCGACATCTGCACTGGCCAGAAATGTAAG 1050
QY 903 GACCTGAGACAGATACAGACAGCACTGAGCACTGAGCCCAACCAATCAGAGATCATC 962
DB 1051 GACCTGAGACAGATACAGACAGCACTGAGCACTGAGCCCAACCAATCAGAGATCATC 1110
QY 963 GCGAGCTTGAAGAGCACTGACAGAGGCTGCTGCGGAGGCTGCTGCGGAGGCTGCTG 1022
DB 1111 GCGAGCTTGAAGAGCACTGACAGAGGCTGCTGCGGAGGCTGCTGCGGAGGCTGCTG 1170
QY 1023 CCGGCTGCGGCGGCGGCGGCTGACCAACGACCACTGACCAACGACATCATCAACAGATC 1082
DB 1171 CCGGCTGCGGCGGCGGCGGCTGACCAACGACCACTGACCAACGACATCATCAACAGATC 1230
QY 1083 TCTACCAAGAGATCCAGAGTGAACGAAACCTGAGGTGTGACACCCCTCTGCTCCACT 1142
DB 1231 TCTACCAAGAGATCCAGAGTGAACGAAACCTGAGGTGTGACACCCCTCTGCTCCACT 1290
QY 1143 ATGCCCACTCTACACAGCTCTCCACTCTTCCACCGAACAGGCCCTGCGGAGAGAGAG 1202
DB 1291 ATGCCCACTCTACACAGCTCTCCACTCTTCCACCGAACAGGCCCTGCGGAGAGAGAG 1350
QY 1203 TGCCCTGAGGCGCTGAGAGTGAAGCAGCAGCAGCTCATCTAAGTGTGAAGCCGAG 1262
DB 1351 TGCCCTGAGGCGCTGAGAGTGAAGCAGCAGCAGCTCATCTAAGTGTGAAGCCGAG 1410
QY 1263 AACACCAACGCTCATGACAGGTGTGTGTCGACAGAGACAGAACCCCGGGGGCTGAGAC 1322
DB 1411 AACACCAACGCTCATGACAGGTGTGTGTCGACAGAGACAGAACCCCGGGGGCTGAGAC 1470
QY 1232 GTCAATCAGAGAGCGCTGATGCTGTGTAATCTTCTCAGAACTGGAGAGCTGACAG 1382
DB 1471 GTCAATCAGAGAGCGCTGATGCTGTGTAATCTTCTCAGAACTGGAGAGCTGACAG 1530
QY 1383 CAAGGCTTGGGAACATTTGACGAGATGCTGCTGAGGCTGAGAAATTTACTGCTG 1442
DB 1531 CAAGGCTTGGGAACATTTGACGAGATGCTGCTGAGGCTGAGAAATTTACTGCTG 1590
QY 1443 ACGAACAAGCAATCAATCAATCTGCTGAGACATGAGAGATGCTGCGGCGGCAAGTGC 1502
DB 1591 ACGAACAAGCAATCAATCAATCTGCTGAGACATGAGAGATGCTGCGGCGGCAAGTGC 1650
QY 1503 TTTGACAGATACGCAAGTTTCCGCTGGAACCTGAGACGAGATTTAAAGCTGCGCTG 1562
DB 1651 TTTGACAGATACGCAAGTTTCCGCTGGAACCTGAGACGAGATTTAAAGCTGCGCTG 1710
QY 1563 GGGCGCTACCATGACATGCGGAGTACTCTTTTACATGAGCAACGCGCAAGAGTGAAC 1622
DB 1711 GGGCGCTACCATGACATGCGGAGTACTCTTTTACATGAGCAACGCGCAAGAGTGAAC 1770
QY 1623 ACCCTGACAGAGATCATGATGTCTACACAGAAACTGTGCGCACTACAGAAAGGAGGC 1682
DB 1771 ACCCTGACAGAGATCATGATGTCTACACAGAAACTGTGCGCACTACAGAAAGGAGGC 1830
QY 1663 TGTGTATTAACGCTGCTGCTCACTCAACCTCAACGAGGCTGTGTACCGGCGGCGCAT 1742
DB 1831 TGTGTATTAACGCTGCTGCTCACTCAACCTCAACGAGGCTGTGTACCGGCGGCGCAT 1890
QY 1743 TACCGAGCGGCTACAGAGACGAGATCTAGGCTGAGTTCAGAGAGGCTCTTACTCA 1802

Db 1891 TACCGAGCGGCTACAGAGCGAGTCTAGTGGGCTGAGTCCAGAGAGGCTCTACTCA 1950
 Qy 1803 CTCAGAAAGGTGTGATGATTCGAGACCCCAACCTTCCACTAGCCAGCTCC 1862
 Db 1951 CTCAGAAAGGTGTGATGATTCGAGACCCCAACCTTCCACTAGCCAGCTCC 2010
 Qy 1863 CCTCTGACCTCTGTCGACATTCGAGAGCCCAACCTTGTACGCTGAGCCAGAGC 1922
 Db 2011 CCTCTGACCTCTGTCGACATTCGAGAGCCCAACCTTGTACGCTGAGCCAGAGC 2070
 Qy 1923 AAGAAACAACCTCTCAACCACTTCTGAGGCTGGAGAGACCGGAGATGCTGATTCGT 1982
 Db 2071 AAGAAACAACCTCTCAACCACTTCTGAGGCTGGAGAGACCGGAGATGCTGATTCGT 2130
 Qy 1983 TTTCCGAGTCACTGAGGAGATGATGAACTGAATCGATACGATTTTCTGCTCC 2042
 Db 2131 TTTCCGAGTCACTGAGGAGATGATGAACTGAATCGATGATGATTTCTGCTCC 2190
 Qy 2043 TACTTCTTCAACACGAGAGCCCTCTCATGTCTCAGAGACGAGACGACTACAGACA 2102
 Db 2191 TACTTCTTCAACACGAGAGCCCTCTCATGTCTCAGAGACGAGACGACTACAGACA 2250
 Qy 2103 CTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2141
 Db 2251 CTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2289

RESULT 8
 ABS65529
 ID ABS65529 standard; cDNA; 2290 BP.
 AC ABS65529;
 XX
 DT 15-NOV-2002 (first entry)
 DE Human TIE ligand NL1 gene.
 XX
 KM Human; TIE ligand NL4; vascularisation; wound healing; heart; limb;
 KM ischaemic condition; vulnerability; vasotropic; gene therapy; NL1; NL5; NL8;
 KM gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6413770-B1.
 PD 02-JUL-2002.
 XX
 PF 19-AUG-1998; 98US-00136801.
 XX
 PR 19-SEP-1997; 97US-00933821.
 PR 29-OCT-1997; 97US-00960507.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Godowski P, Gurney A, Hillan KJ, Botstein D, Goddard A, Roy M,
 PI Ferrara N, Tumas D, Schwall R;
 XX
 DR MPI; 2002-641562/69.
 DR P-PSDB; ABS80355.
 XX
 PT Novel isolated nucleic acid molecules encoding NL4 TIE ligand homologue
 PT polypeptides which are useful for inducing vascularization for wound
 PT healing and treating ischemic condition of the heart or a limb.
 XX
 PS Example 1; Fig 2; 85pp; English.
 XX
 CC The present invention relates to a new nucleic acid molecule which
 CC comprises nucleotides 215 to 1252 of fully defined TIE ligand NL4
 CC polynucleotide sequence of 2212 base pairs as given in the specification.
 CC The nucleic acid of the invention encodes NL4 TIE ligand homologue
 CC polypeptide. The invention is useful for expressing NL4 TIE ligand
 CC homologue polypeptide by recombinant techniques. TIE ligand homologue
 CC polypeptide is useful for inducing vascularisation for promoting wound

CC healing, and for treating ischemic condition of heart or limb. The
 CC present nucleic acid sequence encodes a human TIE ligand protein, as
 CC described in the invention
 XX
 SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
 Query Match 98.1%; Score 2132.6; DB 6; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 AAATGAGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 62
 Db 151 AAATGAGGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 210
 Qy 63 GCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 122
 Db 211 GCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 270
 Qy 123 ACCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 182
 Db 271 ACCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 330
 Qy 183 GAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 242
 Db 331 GAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 390
 Qy 243 AGGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
 Db 391 AGGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 450
 Qy 303 AGCCAAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
 Db 451 AGCCAAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 510
 Qy 363 GCAAAAGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 422
 Db 511 GCAAAAGCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 570
 Qy 423 GAGGCTGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 482
 Db 571 GAGGCTGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 630
 Qy 483 TTCAATTAACCTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
 Db 631 TTCAATTAACCTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 690
 Qy 543 TTCAATTAACCTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 602
 Db 691 TTCAATTAACCTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 750
 Qy 603 GTGCTTCTGAGAGACCGAGTGAATAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
 Db 751 GTGCTTCTGAGAGACCGAGTGAATAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 810
 Qy 663 AAGCAGAAACGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
 Db 811 AAGCAGAAACGAGAGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 870
 Qy 723 AAGCAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
 Db 871 AAGCAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
 Qy 783 TACATGAGCTCTGAGAGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 842
 Db 931 TACATGAGCTCTGAGAGAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 990
 Qy 843 CTGAGAAACAGATCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 902
 Db 991 CTGAGAAACAGATCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1050
 Qy 903 GACCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
 Db 1051 GACCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1110

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QY 963 GGGCAGCTTGAAGAGCACTGCCAGAGGGTGCCTTGGCCAGGCCCTGCCCAAGCCACC 1022
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Db 1171 CCCGCTGCCGCCGCCCGGGTCTACCAACACCCCACTTCAACACCGCATCATCAACAGATC 1230
QY 1083 TCTACCAACAGATCCAGATGACCAAGAACTGAAAGTGTGCGACCCCTCTGCGCACT 1142
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Db 1291 ATGCCCACTCTACAGAGCTCCATCTTCCACCGCAAGCGGTGGGGCCCATGAGAGAC 1350
QY 1203 TGCCTGAGGCCCTGGAGAGTGGCCACGACACAGCTCCATCTACTGTGTGAAGCCGAG 1262
Db 1351 TGCCTGAGGCCCTGGAGAGTGGCCACGACACAGCTCCATCTACTGTGTGAAGCCGAG 1410
QY 1263 AACACCAACCGCTCATGAGAGTGTGTGTGCGACCAAGACAGACACCCCGGGGGCTGAGAC 1322
Db 1411 AACACCAACCGCTCATGAGAGTGTGTGTGCGACCAAGACAGACACCCCGGGGGCTGAGAC 1470
QY 1323 GTCATCCAGAGAGCGCTGGATGGCTCTGTACTTCTTCAAGAACTGGAGAACTGAGTACG 1382
Db 1471 GTCATCCAGAGAGCGCTGGATGGCTCTGTACTTCTTCAAGAACTGGAGAACTGAGTACG 1530
QY 1383 CAAGGCTTTGGGAACTTGAACGCGCAATPCTGGCTGGGCTGGAGAACTTACTGTGCTG 1442
Db 1531 CAAGGCTTTGGGAACTTGAACGCGCAATPCTGGCTGGGCTGGAGAACTTACTGTGCTG 1590
QY 1443 AGCAACCAAGAGCACTACAACTCTGTGACCAATGAGAGATGGTGGCGCGCAAAATG 1502
Db 1591 AGCAACCAAGAGCACTACAACTCTGTGACCAATGAGAGATGGTGGCGCGCAAAATG 1650
QY 1503 TTTGAGAAATACGCGAGTTTCCGCTGGAACCTGAGAGAGATATTATTAAGCTGGAGCTG 1562
Db 1651 TTTGAGAAATACGCGAGTTTCCGCTGGAACCTGAGAGAGATATTATTAAGCTGGAGCTG 1710
QY 1563 GGGCGCTACATGAGCAATGCGGTGATCTCTTTAATGAGCAAAAGGCAAGATTTAC 1622
Db 1711 GGGCGCTACATGAGCAATGCGGTGATCTCTTTAATGAGCAAAAGGCAAGATTTAC 1770
QY 1623 ACCCTGACAGAGATCATGATGTCTTACACAGAACTGTGCCACTTACACAGAGGAGG 1682
Db 1771 ACCCTGACAGAGATCATGATGTCTTACACAGAACTGTGCCACTTACACAGAGGAGG 1830
QY 1683 TGGTGTATTAACGCGCTGTGCCCACTTCAACGCGGTGTGTTATCCGCGGGGCCAT 1742
Db 1831 TGGTGTATTAACGCGCTGTGCCCACTTCAACGCGGTGTGTTATCCGCGGGGCCAT 1890
QY 1743 TACCGGAGCGGTATACAGAGAGAGGCTCTGTGGCTGAGTTCCGAGAGAGCTTACTCA 1802
Db 1891 TACCGGAGCGGTATACAGAGAGAGGCTCTGTGGCTGAGTTCCGAGAGAGCTTACTCA 1950
QY 1803 CTCAGAAAGTGTATGATGATCCGACGGAACCCCAACACCTTCCACTAAGCCAGCTTC 1862
Db 1951 CTCAGAAAGTGTATGATGATCCGACGGAACCCCAACACCTTCCACTAAGCCAGCTTC 2010
QY 1863 CCTCTGAGCTCTGTGGCGCACTTGGCAGAGAGCCCACTGTGTACAGCTGGGCAAGAGAC 1922
Db 2011 CCTCTGAGCTCTGTGGCGCACTTGGCAGAGAGCCCACTGTGTACAGCTGGGCAAGAGAC 2070
QY 1923 AAAGAACAACTCTTCAACAGATTCCTTCAAGCTGTGAGAGACCGGAGATGCTGATTCGT 1982
Db 2071 AAAGAACAACTCTTCAACAGATTCCTTCAAGCTGTGAGAGACCGGAGATGCTGATTCGT 2130
QY 1983 TTTCCGAAGTCACTGACGAGATGATGGAATGGAATCAATAGAGTTTCTGTCCCTCC 2042
Db 2131 TTTCCGAAGTCACTGACGAGATGATGGAATGGAATCAATAGAGTTTCTGTCCCTCC 2190

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QY 2043 TACTTCCCTCACACGACGAGCCCTCATGTCTCCAGACAGAGACTACAGACAA 2102
Db 2191 TACTTCCCTCACACGAGAGCCCTCATGTCTCCAGACAGAGACTACAGACAA 2250
QY 2103 CTCTTTCTTTAAATTAATTAAGTCTCTACAAATTAATA 2141
Db 2251 CTCTTTCTTTAAATTAATTAAGTCTCTACAAATTAATA 2289

RESULT 9
AAD31563
ID AAD31563 standard; DNA; 2290 BP.
XX
AC AAD31563;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human TIE ligand NLI DNA.
XX
KW Human; TIE ligand; NLI; cytoskeletal; osteopathic; vascularisation; toxin;
KW muscular; immunoassay; therapeutic; anti-tumour agent; muscle growth;
KW bone development; maturation; angiogenesis; ds.
XX
OS Homo sapiens.
XX
FX
FH Key Location/Qualifiers
FT CDS 520..2001
FT /tag= a
FT /product= "Human NLI protein"
XX
PN US6350450-B1.
XX
PD 26-FEB-2002.
XX
PE 19-AUG-1998; 98US-00136828.
XX
PR 19-SEP-1997; 97US-0059588P.
XX
PA (GENT) GENENTECH INC.
XX
PI Godowski PJ, Gurney AL, Goddard A, Hillan K;
XX
DR WPI, 2002-215264/27.
XX
DR P-PSDB; AAEL19825.
XX
PT Novel isolated antibody which specifically binds to a mammalian NLI TIE
PT ligand useful for immunoassays, delivery of cytotoxic molecules and as
PT diagnostic agents to detect disease states.
XX
PS Claim 12, Fig 2; 59pp; English.
XX
CC The invention relates to an isolated antibody which specifically binds to
CC a mammalian NLI TIE (Tyrosine kinase containing Ig and EGF homology
CC domains) ligand polypeptide which is capable of inducing vascularisation.
CC The isolated antibody may be used in immunoassays to measure the amount
CC of a TIE ligand in a biological sample. Additionally, the antibody may be
CC used for the delivery of cytotoxic molecules, e.g. radioisotopes or
CC toxins, or therapeutic agents to cells expressing a corresponding TIE
CC receptor. The therapeutic agents may, for example, be other TIE ligands,
CC including the TIE-2 ligand, members of the vascular endothelial growth
CC factor (VEGF) family, or known anti-tumour agents, and agents known to be
CC associated with muscle growth or development, or bone development,
CC maturation, or growth. Anti-TIE ligand antibodies are also suitable as
CC diagnostic agents, to detect disease states associated with the
CC expression of a TIE (e.g. TIE-2) receptor. These detectably labelled
CC antibody agonists of a TIE receptor can be used for imaging the presence
CC of angiogenesis. The present sequence is human TIE ligand NLI DNA
XX
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
Query Match 98.1%; Score 2132.6; DB 6; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY	3	AAATGAGCTGTGCGAGACGGCTGATGAAACCCCAAGCCCTGAGACTGCGAGCGTG	62
Db	151	AAATGAGCTGTGCGAGACGGCTGATGAAACCCCAAGCCCTGAGACTGCGAGCGTG	210
OY	63	GCATGAGGACAGCGGCTGACGCTACTGTGTAGGGAAAGAGGTGTGACACAGCCCGCAGG	122
Db	211	GCATGAGGACAGCGGCTGACGCTACTGTGTAGGGAAAGAGGTGTGACACAGCCCGCAGG	270
OY	123	AACCCCTGGCCAGCCCTGGGCCAGCCTCTGGCCGAGGCCCTCTGTGAGAGCAGAGCAATG	182
Db	271	AACCCCTGGCCAGCCCTGGGCCAGCCTCTGGCCGAGGCCCTCTGTGAGAGCAGAGCAATG	330
OY	183	GAGCCCACTGAGGACAGGCGCTGTGTGGCAGCCACCGGCTTGCACACTCAGAACCCCTCCAG	242
Db	331	GAGCCCACTGAGGACAGGCGCTGTGTGGCAGCCACCGGCTTGCACACTCAGAACCCCTCCAG	390
OY	243	AGGCCATGAGACAGCTGCCCCGAGCTGACGCGCAGGGTGAAGATGTGAAGAGCGGCCCGG	302
Db	391	AGGCCATGAGACAGCTGCCCCGAGCTGACGCGCAGGGTGAAGATGTGAAGAGCGGCCCGG	450
OY	303	AGCCAGACAGAGGGAGAGGCTTTCAATAGATTCTATTCAACAGAAATTAACCACTTTT	362
Db	451	AGCCAGACAGAGGGAGAGGCTTTCAATAGATTCTATTCAACAGAAATTAACCACTTTT	510
OY	363	GCAAGAACAATGAGGCCACTGTGCGTGAACATGCTGTGACTCGAGACTCTGGTCCATG	422
Db	511	GCAAGAACAATGAGGCCACTGTGCGTGAACATGCTGTGACTCGAGACTCTGGTCCATG	570
OY	423	GGAAGCTGTGCAAGCCAGAGAGACGGTTTGTAGGGCACTGAGAGAGGCTCCGCAAGAGAG	482
Db	571	GGAAGCTGTGCAAGCCAGAGAGACGGTTTGTAGGGCACTGAGAGAGGCTCCGCAAGAGAG	630
OY	483	TTCAATTATCTAAACAGGTACAAAGCGGGCGGGCAGGTCCCAAGACAACTGACCTAACCC	542
Db	631	TTCAATTATCTAAACAGGTACAAAGCGGGCGGGCAGGTCCCAAGACAACTGACCTAACCC	690
OY	543	TTCAATTGTGCCCCAGCAGCGGGTCAAGGGTGTGCATCTGCGTCACTCCAGAGGCTGAG	602
Db	691	TTCAATTGTGCCCCAGCAGCGGGTCAAGGGTGTGCATCTGCGTCACTCCAGAGGCTGAG	750
OY	603	GTCGCTTCGAGGAACCGAGTGCATTAAGAGAGAGGCTGAGCTGTCAACATGAGGTGTC	662
Db	751	GTCGCTTCGAGGAACCGAGTGCATTAAGAGAGAGGCTGAGCTGTCAACATGAGGTGTC	810
OY	663	AAGCAGAAAGCGGCAGATGTGAACGCTGCAAGCAAGCTGTGAAGGTGACGCGCATTTTG	722
Db	811	AAGCAGAAAGCGGCAGATGTGAACGCTGCAAGCAAGCTGTGAAGGTGACGCGCATTTTG	870
OY	723	AGCGAGGTGAAGCTCTGCGCAAGGAGAGCGCAACATGAATCGCGGGTCAAGCAAGTTC	782
Db	871	AGCGAGGTGAAGCTCTGCGCAAGGAGAGCGCAACATGAATCGCGGGTCAAGCAAGTTC	930
OY	783	TACATGCAAGCTCTGCAAGAGATCATCCGCAAGCGGGACAACCGGTTTGAAGCTTCCAG	842
Db	931	TACATGCAAGCTCTGCAAGAGATCATCCGCAAGCGGGACAACCGGTTTGAAGCTTCCAG	990
OY	843	CTGAGGAACAGGATCTTGAACCAAGCAGCCAGATGTGTCAGCTGGCGCAGAGATACAG	902
Db	991	CTGAGGAACAGGATCTTGAACCAAGCAGCCAGATGTGTCAGCTGGCGCAGAGATACAG	1050
OY	903	GACCTGAGCAACAATACAGACCTTGGGCACTGGGCCCACTGGGCCCAACAATCAGAGTCAATC	962
Db	1051	GACCTGAGCAACAATACAGACCTTGGGCACTGGGCCCACTGGGCCCAACAATCAGAGTCAATC	1110
OY	963	GCGCAGCTTGAAGAGCACTGCGCAAGAGGTTGCTTGGCGCAAGGCCCGTCCCGACGACCC	1022
Db	1111	GCGCAGCTTGAAGAGCACTGCGCAAGAGGTTGCTTGGCGCAAGGCCCGTCCCGACGACCC	1170
OY	1023	CCCGCTGCCCCCGCCGGCTTACCAACCACTTAACAACCGCATATTAACAACGATC	1082
Db	1171	CCCGCTGCCCCCGCCGGCTTACCAACCACTTAACAACCGCATATTAACAACGATC	1230

RESULT 10
ACD23986
ID ACD23986 standard; cDNA, 2290 BP.
XX
AC ACD23986;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO196 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infectivity; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioindicator; tissue typing; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US0052230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018822.
PR 14-SEP-1998; 98WO-US019099.
PR 14-SEP-1998; 98WO-US019177.
PR 14-SEP-1998; 98WO-US019330.
PR 16-SEP-1998; 98WO-US019437.
PR 17-SEP-1998; 98WO-US021141.
PR 07-OCT-1998; 98WO-US022999.
PR 29-OCT-1998; 98WO-US023922.
PR 29-OCT-1998; 98WO-US024855.
PR 20-NOV-1998; 98WO-US025108.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00809689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017803.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI, 2003-341980/32.
DR P-PSDB; ABO17749.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, acquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 2; Fig 267; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which

Query Match	98.1%;	Score 2132.6;	DB 7;	Length 2290;
Best Local Similarity	.99.8%;	Pred. No. 0;		
Matches 2135; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

Db	811	AAGCAGAAAGCCGAGATGAGACCGCTGGAGACTGGATGGAGGTGCGACCGCGGCAATTGTC	870
Qy	723	AGCCAGGTGAAGCTGTCTGCGCAAGGAGACCGGCAATGAACTGCGGGTCAAGCACTC	782
Db	871	AGCGGGGTGAAGCTGTGCGCGCAAGAGCGCGCAATGAATCTCGCGGTCAAGCACTC	930
Qy	783	TACATGACAGCTCTGTGACGAGATCATCGCAAGCGGGGCAACCGGCTTGAGACTCTCCAG	842
Db	931	TACATGACAGCTCTGTGACGAGATCATCGCAAGCGGGGCAACCGGCTTGAGACTCTCCAG	990
Qy	843	CTGGAGAACAGAGATCTGGAACCAAGCCGACATGCTGAGCTGCGCAGCAAGTACAG	902
Db	991	CTGGAGAACAGAGATCTGGAACCAAGCCGACATGCTGAGCTGCGCAGCAAGTACAG	1050
Qy	903	GACCTGGAGCAAGATCTGGAACCAAGCCGACATGCTGAGCTGCGCAGCAAGTACAG	962
Db	1051	GACCTGGAGCAAGATCTGGAACCAAGCCGACATGCTGAGCTGCGCAGCAAGTACAG	1110
Qy	963	GCGAGCTTGAAGAGCACTGCGAGAGGTGCGCTCGGCGAGCGCGCTGCCAGCCACCC	1022
Db	1111	GCGAGCTTGAAGAGCACTGCGAGAGGTGCGCTCGGCGAGCGCGCTGCCAGCCACCC	1170
Qy	1023	CCCGGTGCGCGCGCGCGCGGTCTTACCAACCAACCACTTACACCGGATCATACACAGATC	1082
Db	1171	CCCGGTGCGCGCGCGCGCGGTCTTACCAACCAACCACTTACACCGGATCATACACAGATC	1230
Qy	1083	TCTACCAACGAGATCCAGAGTGAACCAAACTGAAGTGTGCGCACCCCTCTGCCACT	1142
Db	1231	TCTACCAACGAGATCCAGAGTGAACCAAACTGAAGTGTGCGCACCCCTCTGCCACT	1290
Qy	1143	ATGCCACTCTCACAGCTTCCATCTTCCACGACAGCCGTCGGGCGCCATGGAGAGAC	1202
Db	1291	ATGCCACTCTCACAGCTTCCATCTTCCACGACAGCCGTCGGGCGCCATGGAGAGAC	1350
Qy	1203	TGCCTGCGGCGCGCGGAGATGGGCAAGCAACAGCTCCATCTAACCTGGGTGAAGCCGGAG	1262
Db	1351	TGCCTGCGGCGCGCGGAGATGGGCAAGCAACAGCTCCATCTAACCTGGGTGAAGCCGGAG	1410
Qy	1263	AACACCAACCGCCTCATGACGAGTGTGTGTGGACCAAGACACGACCCCGGGGCTGAGCC	1322
Db	1411	AACACCAACCGCCTCATGACGAGTGTGTGTGGACCAAGACACGACCCCGGGGCTGAGCC	1470
Qy	1323	GTCAATCCAGAGACGCTCGATGGCTCTGTTAATCTTTCAGAGAACTGGGAGACGTACAAG	1382
Db	1471	GTCAATCCAGAGACGCTCGATGGCTCTGTTAATCTTTCAGAGAACTGGGAGACGTACAAG	1530
Qy	1383	CAAGGGTTTGAGAAATTTGACAGCGCAATACTGTGCTGAGCCTGGAGAACTTTAATGTGCTG	1442
Db	1531	CAAGGGTTTGAGAAATTTGACAGCGCAATACTGTGCTGAGCCTGGAGAACTTTAATGTGCTG	1590
Qy	1443	ACGAAACCAAGGCAATCTACAACTCTGTGTGACCATGAGAGACTGTGCGGCGCAAGTCT	1502
Db	1591	ACGAAACCAAGGCAATCTACAACTCTGTGTGACCATGAGAGACTGTGCGGCGCAAGTCT	1650
Qy	1503	TTTTCAGAAATTAAGCAAGTTTCCGCGCTGGAAACCTGAAGAGAGATTAATTAAGCTGGGCTG	1562
Db	1651	TTTTCAGAAATTAAGCAAGTTTCCGCGCTGGAAACCTGAAGAGAGATTAATTAAGCTGGGCTG	1710
Qy	1563	GGGCGCTACCATGAGCAATGCGGGTGAATCTCTTTACATGGCAACCGGCAAGCAATTCAAC	1622
Db	1711	GGGCGCTACCATGAGCAATGCGGGTGAATCTCTTTACATGGCAACCGGCAAGCAATTCAAC	1770
Qy	1623	ACCTTGAACAGATATCATATGTCTTCAACAGAAATGTGCCCACTACACAGAAAGGAGGC	1682
Db	1771	ACCTTGAACAGATATCATATGTCTTCAACAGAAATGTGCCCACTACACAGAAAGGAGGC	1830
Qy	1683	TGATGTATTAACCTGTGCGCCACTCAACCTCAACGAGGATGTGATCCGCGGAGGCAAT	1742
Db	1831	TGATGTATTAACCTGTGCGCCACTCAACCTCAACGAGGATGTGATCCGCGGAGGCAAT	1890
Qy	1743	TACCGAGCCGCTTACAGAGCGGAGTCTACTGGGCTGAGTTCGAGAGAGCTCTTAATCTCA	1802

PR 02-VAR-2000; 2000MO-US005746.

PA (GERTH) GENENTECH INC.

XX Baker KP, Beresini W, Deforge L, Desnoyers L, Filiaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;

XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhong Z;

DR WPI: 2003-352836/33.

DR P-PSDB; AB081003.

XX New isolated PRO polypeptide useful for treating diabetes, rheumatoid

PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or

XX heart attack.

XX Claim 2; Fig 267; 643pp; English.

XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ACA6599-ACA67268 represent cDNA sequences encoding
CC the human PRO polypeptides of the invention. Note: The sequence data for
CC this patent was obtained in electronic format directly from the USPTO web
CC site at seqdata.uspto.gov/bispidbentry.html

XX Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match 98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2155; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AAATGAGCTGCTCGGACGCGCTTGAAGTGAATCCCAAGCCCTTGAGCTTCCGAGCTG 62
DB 151 AATGAGGCTGCTCGGACGCGCTTGAAGTGAATCCCAAGCCCTTGAGCTTCCGAGCTG 210
QY 63 GGACGTGAGGCGAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 122
DB 211 GACTGTGAGGCGAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 270
QY 123 ACCCTTGAGGCGAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 182
DB 271 ACCCTTGAGGCGAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 330
QY 183 GAGCCCAAGTGAAGGAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 242
DB 331 GAGCCCAAGTGAAGGAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 390
QY 243 AGGCGATGAGCAAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 302
DB 391 AGGCGATGAGCAAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 450
QY 303 AGGCGATGAGCAAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 362
DB 451 AGGCGATGAGCAAGGCTGCGCTACTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 510
QY 363 GGAAGAGCAGTGAAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 422
DB 511 GGAAGAGCAGTGAAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 570
QY 423 GGAAGAGCAGTGAAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 482
DB 571 GGAAGAGCAGTGAAGGCTGTTGAGGAGAAAGAGTTGTTGAGCAAGCCCGCAGG 630
QY 483 TTCAATTTACCTTAAGAGTGAAGGCGGCGGCTGCGCAAGCAATGAGCAATCAACC 542
DB 631 TTCAATTTACCTTAAGAGTGAAGGCGGCGGCTGCGCAAGCAATGAGCAATCAACC 690

QY 543 TTCAATTTACCTTAAGAGTGAAGGCGGCGGCTGCGCAAGCAATGAGCAATCAACC 602
DB 691 TTCAATTTACCTTAAGAGTGAAGGCGGCGGCTGCGCAAGCAATGAGCAATCAACC 750
QY 603 GTGCTTCTGAGAGACCGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTGTC 662
DB 751 GTGCTTCTGAGAGACCGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTGTC 810
QY 663 AAGCAGAGGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTGTC 722
DB 811 AAGCAGAGGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTGTC 870
QY 723 AGGAGAGTGAAGCTGCTGCGCAAGAGACCGGCAATGAGCTGCGGCTCAAGCACTC 782
DB 871 AGGAGAGTGAAGCTGCTGCGCAAGAGACCGGCAATGAGCTGCGGCTCAAGCACTC 930
QY 783 TACATGAGTCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 842
DB 931 TACATGAGTCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 900
QY 843 CTGAGAGACAGATCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 902
DB 991 CTGAGAGACAGATCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 1050
QY 903 GACCTGAGACAGATCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 962
DB 1051 GACCTGAGACAGATCTCTGCAAGAGATCATCCGCAAGCGGCAATGAGCTTCCCG 1110
QY 963 GGGCAGCTTGAAGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1022
DB 1111 GGGCAGCTTGAAGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1170
QY 1023 CCGCTGAGGCGGCGGCTGCTCAAGAGAGTGAAGCTGCTCAATGAGCTTCCCG 1082
DB 1171 CCGCTGAGGCGGCGGCTGCTCAAGAGAGTGAAGCTGCTCAATGAGCTTCCCG 1230
QY 1083 TCTAAGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1142
DB 1231 TCTAAGAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1290
QY 1143 ATGCCCACTCTCAAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1202
DB 1291 ATGCCCACTCTCAAGAGTGCATTAAGCAGAGTGAAGCTGCTCAATGAGCTTCCCG 1350
QY 1203 TGCCTGAGGCGGCGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1262
DB 1351 TGCCTGAGGCGGCGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1410
QY 1263 AACACCAAGGCGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1322
DB 1411 AACACCAAGGCGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1470
QY 1323 GTGATCAGAGAGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1382
DB 1471 GTGATCAGAGAGGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1530
QY 1383 CAAGGAGTGAAGAGTGAAGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1442
DB 1531 CAAGGAGTGAAGAGTGAAGCTGCTCAAGAGTGAAGCTGCTCAATGAGCTTCCCG 1590
QY 1443 ACGAAGCAAGGCAATCAAGAGTGAAGCTGCTCAAGAGTGAAGCTTCCCG 1502
DB 1591 ACGAAGCAAGGCAATCAAGAGTGAAGCTGCTCAAGAGTGAAGCTTCCCG 1650
QY 1503 TTTGCAAGATTAAGGAGTGAAGCTGCTCAAGAGTGAAGCTTCCCG 1562
DB 1651 TTTGCAAGATTAAGGAGTGAAGCTGCTCAAGAGTGAAGCTTCCCG 1710
QY 1563 GGGCGCTACATGAGCAATGAGGAGTGAAGCTTCAATGAGCAATGAGCAATCAACC 1622
DB 1711 GGGCGCTACATGAGCAATGAGGAGTGAAGCTTCAATGAGCAATGAGCAATCAACC 1770

PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-0087879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Geritsen ME, Goddard A, Godowski PJ, Gunney AU, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX
XX WPI; 2003-332040/31.
DR P-PSDB; ABU66703.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
XX
XX Claim 2; Fig 267; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
CC encoding the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipd/entry.html
XX
SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
Query Match 98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 AAATGAGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCTGAGACTGCCAGCGTG 62
Db 151 AAATGAGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCTGAGACTGCCAGCGTG 210
QY 63 GCACTGAGGCAAGCGGCTGACCTGCTGAGGAGAAAGAGTTGTGACGACGCCGAGG 122
Db 211 GCACTGAGGCAAGCGGCTGACCTGCTGAGGAGAAAGAGTTGTGACGACGCCGAGG 270
QY 123 ACCCTGAGCGAGCCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 182
Db 271 ACCCTGAGCGAGCCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 330
QY 183 GAGCCAGTGAAGCAAGGCTGCTTGGAGCAGCAGCGGCTGCACTCAGAAACCCCTCAG 242
Db 331 GAGCCAGTGAAGCAAGGCTGCTTGGAGCAGCAGCGGCTGCACTCAGAAACCCCTCAG 390
QY 243 AGGCGATGAGAGAGGCTGCGCGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 302
Db 391 AGGCGATGAGAGAGGCTGCGCGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 450

QY 303 AGCCAGAGAGAGAGAGAGGCTTTTCATAGATTCTATTCAGAAAGATTAACCACTTTT 362
Db 451 AGCCAGAGAGAGAGAGAGGCTTTTCATAGATTCTATTCAGAAAGATTAACCACTTTT 510
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Db 511 GCAAAGACATAGAGAGGCACTGTGCGTGAACATGCTGTGAGGCTGCGACTGTGCGCATG 570
QY 423 GAGCTGTTGACGCGCAGAGAGAGCGGTTTGAAGGCACTGAGAGAGGCTTCCAGAGAG 482
Db 571 GAGCTGTTGACGCGCAGAGAGAGCGGTTTGAAGGCACTGAGAGAGGCTTCCAGAGAG 630
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QY 543 TTCAATTGCTCCAGAGAGCGGCTGACGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 602
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Db 811 AAGCAGAGAGGAGATCGAGAGCTGACAGAGCTGTAAGGAGAGCGGAGCTTGTG 870
QY 723 AGGAGGTGAAGCTGCTGCGCAAGAGAGAGCGGCAATGAATCTCGGGGTCAAGAGCTC 782
Db 871 AGGAGGTGAAGCTGCTGCGCAAGAGAGAGCGGCAATGAATCTCGGGGTCAAGAGCTC 930
QY 783 TACATGAGCTCTGACAGAGATCATCCGCAAGCGGCAAGCGGCTGAGGCTTCCAG 842
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Db 991 CTGAGAAAGAGATCTCTGAACAGAGAGCGGCAATGCTGAGCTGAGCGAGATCAAG 1050
QY 903 GACCTGAGAGCAAGTACAGAGAGCTGCGCAAGCTGCGGCAAGCTGCGGCAAGTACAG 962
Db 1051 GACCTGAGAGCAAGTACAGAGAGCTGCGCAAGCTGCGGCAAGCTGCGGCAAGTACAG 1110
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Db 1231 TCTACCAAGAGATCCAG 1290
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Db 1291 ATGCCACTTCTACAGAGCTTCCATCTTCAACGAGAGAGAGAGAGAGAGAGAGAG 1350
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Db 1351 TGCGTGAAG 1410
QY 1263 AACACCAACCGGCTCATGAGAGTGTGTGCGACAGAGAGAGAGAGAGAGAGAGAGAG 1322
Db 1411 AACACCAACCGGCTCATGAGAGTGTGTGCGACAGAGAGAGAGAGAGAGAGAGAGAG 1470
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Db 1471 GTCATTCAG 1530

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QY 1443 ACGAACCAAGCACTAATACTCTGTGTGACCATGAGAGACTGGTCCGCGCAAGTC 1502
    |||
Db 1591 ACGAACCAAGCACTAATACTCTGTGTGACCATGAGAGACTGGTCCGCGCAAGTC 1650
QY 1503 TTGGAGATAGCGCAGTTTCCGCTGGAACTGTGAGACGAGTATTTATAGCTGGGCTG 1562
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Db 1651 TTGGAGATAGCGCAGTTTCCGCTGGAACTGTGAGACGAGTATTTATAGCTGGGCTG 1710
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Db 1711 GGGCGCTACCATGGCAATGCGGGTGACTCTTTACATGGCAACAGGCAAGCTTCAAC 1770
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QY 1863 CCTCTCTGACCTCTGTGTGCGCAATTCGACAGAGCCACCTGTGTCACTGTGCGCACAGCAG 1922
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Db 2011 CCTCTCTGACCTCTGTGTGCGCAATTCGACAGAGCCACCTGTGTCACTGTGCGCACAGCAG 2070
QY 1923 AAAAGAACACTCTCTACACAGTTCATCTGAGGCTGGGAGACCGGGAGTGTGATTTCTGT 1982
    |||
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QY 2043 TACTTCTCTCAACCAAGACGCGCTCATGTCTCCAGACAGACAGAGTACAGACAA 2102
    |||
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QY 2103 CTCTTCTTAAATAATTAAGTCTCTCAATAAATAACA 2141
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Db 2251 CTCTTCTTAAATAATTAAGTCTCTCAATAAATAAATA 2289

RESULT 14
ACAA04921
ID ACAA04921 standard; cDNA; 2290 BP.
XX
ACAA04921:
XX
DE Novel human secreted and transmembrane protein PRO196 cDNA.
XX
DT 28-MAY-2003 (first entry)
XX
KW Secreted and transmembrane polypeptide; PRO polypeptide; PRO533; PRO301;
KW PRO187; PRO337; PRO1411; PRO10956; PRO245; PRO6307; PRO6003; PRO6004;
KW PRO4356; PRO2630; PRO265; PRO941; FGR; bioactive molecule;
KW fibroblast growth factor receptor; cell death; chromosome mapping;
KW gene mapping; transgenic animal; knockout animal; gene therapy; tumour;
KW obesity; diabetes; insulinemia; vascular permeability;
KW cardiac insufficiency disorder; immune response; hearing loss;
KW auditory hair cell regeneration; bone disorder; cartilage disorder;
KW sports injury; arthritis; gene; ss.
XX
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OS Homo sapiens.
XX
PN US2003032063-A1.
XX
PD 13-FEB-2003.
XX
PF 01-FEB-2002; 2002US-00066494.
XX
26-AUG-1997; 97US-0056974P.
PR 17-SEP-1997; 97US-0059115P.
PR 18-SEP-1997; 97US-0059263P.
PR 19-SEP-1997; 97US-0059588P.
PR 17-OCT-1997; 97US-0062285P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063082P.
PR 27-OCT-1997; 97US-0063329P.
PR 29-OCT-1997; 97US-0063733P.
PR 21-NOV-1997; 97US-0066364P.
PR 23-NOV-1997; 97US-0066840P.
PR 16-DEC-1997; 97US-0069594P.
PR 09-FEB-1998; 97US-0074086P.
PR 09-FEB-1998; 97US-0074092P.
PR 25-MAR-1998; 97US-0079294P.
PR 08-APR-1998; 97US-0081049P.
PR 10-AUG-1998; 97US-0095598P.
PR 18-AUG-1998; 97US-0097000P.
PR 09-SEP-1998; 97US-0099601P.
PR 10-SEP-1998; 97US-0099803P.
PR 10-SEP-1998; 97US-0099811P.
PR 10-SEP-1998; 97US-0099812P.
PR 14-SEP-1998; 97US-0099812P.
PR 16-SEP-1998; 97US-0099812P.
PR 17-SEP-1998; 97US-0100858P.
PR 17-SEP-1998; 97US-01019437.
PR 24-SEP-1998; 97US-01019437.
PR 28-OCT-1998; 97US-0106032P.
PR 20-NOV-1998; 97US-0109304P.
PR 20-NOV-1998; 97US-0109304P.
PR 25-NOV-1998; 97US-0109304P.
PR 01-DEC-1998; 97US-0109304P.
PR 08-MAR-1999; 97US-0109304P.
PR 23-MAR-1999; 97US-0109304P.
PR 02-JUN-1999; 97US-0109304P.
PR 15-JUN-1999; 97US-0109304P.
PR 20-JUL-1999; 97US-0145070P.
PR 26-JUL-1999; 97US-0145070P.
PR 17-AUG-1999; 97US-0145070P.
PR 01-SEP-1999; 97US-0145070P.
PR 08-SEP-1999; 97US-0145070P.
PR 15-SEP-1999; 97US-0145070P.
PR 15-SEP-1999; 97US-0145070P.
PR 30-NOV-1999; 97US-0145070P.
PR 01-DEC-1999; 97US-0145070P.
PR 02-DEC-1999; 97US-0145070P.
PR 07-DEC-1999; 97US-0145070P.
PR 20-DEC-1999; 97US-0145070P.
PR 05-JAN-2000; 97US-0145070P.
PR 18-FEB-2000; 97US-0145070P.
PR 18-FEB-2000; 97US-0145070P.
PR 22-FEB-2000; 97US-0145070P.
PR 01-MAR-2000; 97US-0145070P.
PR 02-MAR-2000; 97US-0145070P.
PR 09-MAR-2000; 97US-0145070P.
PR 20-MAR-2000; 97US-0145070P.
PR 30-MAR-2000; 97US-0145070P.
PR 15-MAY-2000; 97US-0145070P.
PR 17-MAY-2000; 97US-0145070P.
PR 22-MAY-2000; 97US-0145070P.
PR 30-MAY-2000; 97US-0145070P.
PR 02-JUN-2000; 97US-0145070P.
PR 11-AUG-2000; 97US-0145070P.
PR 23-AUG-2000; 97US-0145070P.
PR 24-AUG-2000; 97US-0145070P.
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PR 01-DEC-2000; 2000MO-US032678.
PR 28-FEB-2001; 2001MO-US006520.
PR 30-MAY-2001; 2001MO-US017443.
PR 01-JUN-2001; 2001MO-US017800.
PR 20-JUN-2001; 2001MO-US019692.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 15-NOV-2001; 2001US-00002796.
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein DA, Desnovers L, Eaton DL;
PI Ferreira N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kijavitt J, Mather JP, Napier MA, Pan J;
PI Paoli NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX WPI; 2003-341964/32.
DR P-PSDB; AB067268.
XX
XX Thirty seven nucleic acids encoding novel secreted and transmembrane PRO
PT polypeptides, useful for modulating biological activity of cell
PT expressing the polypeptide, and in chromosome and gene mapping.
XX
XX Claim 2; Fig 1; 255pp; English.
XX
XX The invention describes an isolated, secreted and transmembrane
CC polypeptide (I), termed PRO polypeptide. (II) is useful for detecting
CC PRO33, PRO301, PRO187, PRO337, PRO411, PRO10095, PRO246, PRO6307,
CC PRO6003, PRO6004, PRO4356, PRO2630, PRO265, PRO941, fibroblast growth
CC factor receptor (FGFR)-4, FGFR-3, FGFR-2 or FGFR-1 polypeptide, and for
CC linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a
CC cell expressing the polypeptides. The bioactive molecule causes cell
CC death. (III) is useful as hybridisation probes, in chromosome and gene
CC mapping, in generation of antisense RNA and DNA, in the preparation of
CC PRO polypeptide, for generating transgenic animals or knockout animals
CC which in turn are useful in the development and screening of
CC therapeutically useful reagents, and for the genetic analysis of
CC individuals with genetic disorders, in gene therapy, and for chromosome
CC identification. (I) Or Ab is useful for the preparation of medicament for
CC treating conditions which are responsive to the PRO polypeptide or anti-
CC PRO antibody e.g. a tumour. (II) is useful for treating obesity, diabetes
CC or hypo- or hyper-insulinaemia, and cardiac insufficiency disorders, for
CC inhibiting tumour growth, enhances vascular permeability and immune
CC response, for inducing regeneration of auditory hair cells and for
CC treating hearing loss in mammals, and for treating bone and/or cartilage
CC disorders such as sports injuries and arthritis. This sequence encodes a
CC novel human secreted and transmembrane polypeptide associated
CC oligonucleotide
XX
XX Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;
SQ
Query Match 98.1%; Score 2132.6; DB 7; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 AANTAGGCTGCTGGGAGCGGCTGAGATGAACCCCAAGCCCTGGAGCTGCGAGGCTG 62
DB 151 AATATAGGCTGCTGGGAGCGGCTGAGATGAACCCCAAGCCCTGGAGCTGCGAGGCTG 210
QY 63 GCACTGAGGCAAGCGGCTGAGCTGCTGAGGAGAAAGAGTGTGAGCAAGCCCGAGG 122
DB 211 GCACTGAGGCAAGCGGCTGAGCTGCTGAGGAGAAAGAGTGTGAGCAAGCCCGAGG 270
QY 123 ACCCTTGAGCAAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 182
DB 271 ACCCTTGAGCAAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 330
QY 163 GAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
DB 331 GAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 390
QY 243 AGGCAATGAGAGGCTGCGCCCGCTGAGCGGCAAGGAGTGAAGATGTGAGAGAGCCGCCCGG 302

DB 391 AGGCAATGAGAGGCTGCGCCCGCTGAGCGGCAAGGAGTGAAGATGTGAGAGAGCCGCCCGG 450
QY 303 AGCCAAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
DB 451 AGCCAAAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 510
QY 363 GCAAAGCACTAGAGGCACTGTCGTCATGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTC 422
DB 511 GCAAAGCACTAGAGGCACTGTCGTCATGTCGTGTCGTGTCGTGTCGTGTCGTGTCGTGTC 570
QY 423 GGAAGCTGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 482
DB 571 GGAAGCTGTTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 630
QY 483 TTGATTACTTAACAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542
DB 631 TTGATTACTTAACAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 690
QY 543 TTGATTACTTAACAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602
DB 691 TTGATTACTTAACAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 750
QY 603 GTGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
DB 751 GTGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 810
QY 663 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722
DB 811 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 870
QY 723 AGGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
DB 871 AGGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
QY 783 TACATCAGAGTCTGTCAGAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 842
DB 931 TACATCAGAGTCTGTCAGAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 990
QY 843 CTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 902
DB 991 CTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1050
QY 903 GACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
DB 1051 GACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1110
QY 963 GCGCAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
DB 1111 GCGCAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1170
QY 1023 CCGGCTGCGCCCGCCCGGCTTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1082
DB 1171 CCGGCTGCGCCCGCCCGGCTTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1230
QY 1083 TCTACCAAGAGATCCAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAG 1142
DB 1231 TCTACCAAGAGATCCAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAG 1290
QY 1143 ATGCCACTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1202
DB 1291 ATGCCACTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1350
QY 1203 TGCCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1262
DB 1351 TGCCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1410
QY 1263 AACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1322
DB 1411 AACACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1470
QY 1323 GTATCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1382

Db 1471 GTTCATCCAGAGACGCTGGATGGCTCTGTATTAATTCTTCAGGAACCTGGAGACGTACAAAG 1530
QY 1393 CAAGGGTTTGGGACATTGACGGGCGAATACCTGGCTGGGCTGGAGACATTACTAGGCTG 1442
Db 1531 CAAGGGTTTGGGACATTGACGGGCGAATACCTGGCTGGGCTGGAGACATTACTAGGCTG 1590
QY 1443 ACGAACCAAGGCACCTAACTCTGTGTGACCAATGAGAGACTGTGCTGGGCGCAAAATG 1502
Db 1591 ACGAACCAAGGCACCTAACTCTGTGTGACCAATGAGAGACTGTGCTGGGCGCAAAATG 1650
QY 1503 TTTCGAAATAGCCAGATTCCGCTGGAACCTGAGACGAGATATTAATAGCTGGGCTG 1562
Db 1651 TTTCGAAATAGCCAGATTCCGCTGGAACCTGAGACGAGATATTAATAGCTGGGCTG 1710
QY 1563 GGGCGCTACCATGGCAATCGGGTGAATCTTTATCATGGAACAAGCAAGCAATTCACC 1622
Db 1711 GGGCGCTACCATGGCAATCGGGTGAATCTTTATCATGGAACAAGCAAGCAATTCACC 1770
QY 1623 ACCCTGACAGATCATGATGTCTACACAGAAACTGTGCCACTTACCAAGAGGAGGC 1682
Db 1771 ACCCTGACAGATCATGATGTCTACACAGAAACTGTGCCACTTACCAAGAGGAGGC 1830
QY 1683 TGGGTGTAATACGCGCTGGCCCACTCCAACTCAAGGGGTCTGGTACCGGGGGCCAT 1742
Db 1831 TGGGTGTAATACGCGCTGGCCCACTCCAACTCAAGGGGTCTGGTACCGGGGGCCAT 1890
QY 1743 TACCGAGCGGCTACACAGACGAGTCTACTGGGCTGAGTTCCAGAGAGCTTTACTCA 1802
Db 1891 TACCGAGCGGCTACACAGACGAGTCTACTGGGCTGAGTTCCAGAGAGCTTTACTCA 1950
QY 1803 CTCAGAAAGTGTATGATGATCCGACCGAACCACCTTCCACTAAGCCAGCTCC 1862
Db 1951 CTCAGAAAGTGTATGATGATCCGACCGAACCACCTTCCACTAAGCCAGCTCC 2010
QY 1863 CCTCTGACTCTGTGGCCATTCGACGAGACCCACCTGTGTCAGCTGGCCACAGCAC 1922
Db 2011 CCTCTGACTCTGTGGCCATTCGACGAGACCCACCTGTGTCAGCTGGCCACAGCAC 2070
QY 1923 AAAAACAACCTCTCAACCACTTCATCTGAGGCTGGAGAGACCGGAGTCTGATTTCTGT 1982
Db 2071 AAAAACAACCTCTCAACCACTTCATCTGAGGCTGGAGAGACCGGAGTCTGATTTCTGT 2130
QY 1983 TTTCGAGATCACTGACGAGATGATGAATGAATGATGATGATGATGATGATGATGATGAT 2042
Db 2131 TTTCGAGATCACTGACGAGATGATGAATGAATGATGATGATGATGATGATGATGATGAT 2190
QY 2043 TACTTCTCTTCAACACGACAGCCCTCACTGTCTCCAGACAGACAGAGACTACAGACAA 2102
Db 2191 TACTTCTCTTCAACACGACAGCCCTCACTGTCTCCAGACAGACAGAGACTACAGACAA 2250
QY 2103 CTCCTTCTTAAATTAATTAAGTCTCTAATAAATAAACA 2141
Db 2251 CTCCTTCTTAAATTAATTAAGTCTCTAATAAATAAACA 2289

RESULT 15
ABX89274
ID ABX89274 strand: cDNA; 2290 BP.
XX ABX89274;
XX 13-MAY-2003 (first entry)
DE DNA encoding novel secreted and transmembrane protein PRO196.
XX
XX Human, PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW Cardiac insufficiency disorder; cancer; tumor; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;

KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX Homo sapiens.
XX US2003017563-A1.
XX 23-JAN-2003.
PD
PF 07-MAY-2002; 2002US-00140808.
XX 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US006615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028501.
PR 01-DEC-1999; 99WO-US028534.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004432.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004814.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007277.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-DEC-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US074259.
PR 28-FEB-2001; 2001MO-US034956.
PR 28-FEB-2001; 2001MO-US065520.
PR 01-MAR-2001; 2001MO-US066666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001MO-US019682.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001MO-US020116.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908837.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.

(GENE) GENENTECH INC.

BAKER KP, Berezini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
Gerdsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S,
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z,
WPI; 2003-148238/14.
P-PSDB; ABUS9784.

Two hundred and seventy five nucleic acids encoding PRO polypeptides,
useful for treating pericyte-associated tumors, diabetes and various bone
and/or cartilage disorders, e.g. arthritis.

Claim 2; Fig 267; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO
polypeptides are useful in detecting PRO polypeptides in a sample, in
linking a bioactive molecule to a cell expressing a PRO polypeptide, and
in modulating at least one biological activity of a cell expressing a PRO
polypeptide. PRO312 stimulates hypertrophy of neonatal heart and is thus
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
stimulate adrenal cortical capillary endothelial growth, and PRO536,
PRO343, PRO823, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
useful for treating conditions or disorders where angiogenesis would be
beneficial, e.g. wound healing and antagonist of this polypeptide are
useful for treating cancerous tumors. PRO812 inhibits vascular
endothelial growth factor (VEGF) stimulated proliferation of endothelial
cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
PRO1068, PRO1184, PRO1366 and PRO1375 stimulate proliferation of
stimulated T-lymphocytes and are therapeutically useful for enhancing
immune response. PRO828, PRO826, PRO1068 or PRO132 enhance survival of
retinal neurons cells (PRO1132 is also enhances survival/proliferation of
rod photoreceptor cells) and therefore are useful for treating retinal

CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This sequence
CC encodes a novel human PRO protein
XX

SQ Sequence 2290 BP; 537 A; 692 C; 668 G; 393 T; 0 U; 0 Other;

Query Match 98.1%; Score 2132.6; DB 7; Length 2290;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;

Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATGAGGCTGCTGCGAGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 62
DB 151 AATGAGGCTGCTGCGAGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 210
QY 63 GCACTGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 122
DB 211 GCACTGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 270
QY 123 ACCCTGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 182
DB 271 ACCCTGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 330
QY 183 GAGCCAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 242
DB 331 GAGCCAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 390
QY 243 AGGCAAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 302
DB 391 AGGCAAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 450
QY 303 AGGCAAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 362
DB 451 AGGCAAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 510
QY 363 GCAAGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 422
DB 511 GCAAGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 570
QY 423 GAGCTGTTGCAAGGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 482
DB 571 GAGCTGTTGCAAGGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 630
QY 483 TTGATTACTTAACAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 542
DB 631 TTGATTACTTAACAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 690
QY 543 TTGATTACTTAACAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 602
DB 691 TTGATTACTTAACAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 750
QY 603 GTGCTTGTGAGAACCGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 662
DB 751 GTGCTTGTGAGAACCGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 810
QY 663 AAGCAGAGGAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 722
DB 811 AAGCAGAGGAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 870
QY 723 AAGCAGAGGAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 782
DB 871 AAGCAGAGGAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 930
QY 783 TACATGAGTGAAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 842
DB 931 TACATGAGTGAAGGAGTGAAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 990
QY 843 CTGAGAGAGAGATCTGAGAGAGGAGGCGGCTGAGTGAACCCAGCCCTGAGCTGCGGAGCTG 902

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Db 991 CTGGAGAACAGATCTCTGACACGACAGCCGACATGCTGCACTGGCCAGCAATGACAG 1050
Qy 903 GACCTGGAGCACAATACCAAGCACTGGCCCACTGGCCCAACCAATCAAGATCATC 962
Db 1051 GACCTGGAGCACAATACCAAGCACTGGCCCACTGGCCCAACCAATCAAGATCATC 1110
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Db 1111 GCGCAGCTTGAAGGACATGCGCAGAGGGTGGCCCTGGCCAGGCCCGTCCCAAGCCACC 1170
Qy 1023 CCGCGTGGCCCGCCCGGGGTCTACCAACCAACCACTTACCAACCGCATCATCAACCAATC 1082
Db 1171 CCGCGTGGCCCGCCCGGGGTCTACCAACCAACCACTTACCAACCGCATCATCAACCAATC 1230
Qy 1083 TCTACCAACGAGATCCAGATGACACGAACTTGAAGGTGCTGCCACCCCTCTGCCCCACT 1142
Db 1231 TCTACCAACGAGATCCAGATGACACGAACTTGAAGGTGCTGCCACCCCTCTGCCCCACT 1290
Qy 1143 ATGCCACTCTCACAGCCTCCCATCTTCCACCCGACAGCCGTGGGCCCATGGAGAGAC 1202
Db 1291 ATGCCACTCTCACAGCCTCCCATCTTCCACCCGACAGCCGTGGGCCCATGGAGAGAC 1350
Qy 1203 TGCCTGCAAGGCTTGGAGGATGGCCACGACACAGCTCCATCTTACCTGGTGAAGCCGAG 1262
Db 1351 TGCCTGCAAGGCTTGGAGGATGGCCACGACACAGCTCCATCTTACCTGGTGAAGCCGAG 1410
Qy 1263 AACACCAACCGGCTCATGAGGTGTGTGCGACGAGACAGACGACCCCGGGGGCTGGAGC 1322
Db 1411 AACACCAACCGGCTCATGAGGTGTGTGCGACGAGACAGACGACCCCGGGGGCTGGAGC 1470
Qy 1323 GTCATCCAGAGACGCGCTGGATGGCTGTGTAACTTTCAGAGAACTGGAGACGTACAG 1382
Db 1471 GTCATCCAGAGACGCGCTGGATGGCTGTGTAACTTTCAGAGAACTGGAGACGTACAG 1530
Qy 1383 CAAGGCTTGGGAACTTGAACGGCGAATATCGCTGGGGCTGGAGAACTTTACTGGCTG 1442
Db 1531 CAAGGCTTGGGAACTTGAACGGCGAATATCGCTGGGGCTGGAGAACTTTACTGGCTG 1590
Qy 1443 ACGAACCAAGGCACTACAACTCCTGGTGAACATGAGAGACTGGTCCGCGCGCAAAATC 1502
Db 1591 ACGAACCAAGGCACTACAACTCCTGGTGAACATGAGAGACTGGTCCGCGCGCAAAATC 1650
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Search completed: August 6, 2004, 14:23:31
 Job time : 874 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 12:27:03 ; Search time 8364 Seconds

(without alignments)
11260.690 Million cell updates/sec

Title: US-10-018-386-1

Perfect score: 2173

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	2146.2	98.8	2288	6	BD260120	BD260120 Matrix-re
4	2133.2	98.2	3541	6	AX014413	AX014413 Sequence
5	2133.2	98.2	3541	6	BD222237	BD222237 Human nuc
6	2132.6	98.1	2290	6	AR081094	AR081094 Sequence
7	2132.6	98.1	2290	6	AR194809	AR194809 Sequence
8	2132.6	98.1	2290	6	AR205229	AR205229 Sequence
9	2132.6	98.1	2290	6	AR266344	AR266344 Sequence
10	2132.6	98.1	2290	6	AR307688	AR307688 Sequence
11	2132.6	98.1	2290	6	AR350376	AR350376 Sequence
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ALIGNMENTS

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VERSION	AX069013.1	GI:12578633				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
REFERENCE	Friedrich,G., Hagen,G., Wick,M., Zubov,D. and Dubois-Stringfellow,N.					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
TITLE	Methods for modulating angiogenesis by using the anti-angiogenic					

Accession	Sequence	Position
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RESULT 2	LOCUS	DEFINITION	2178 bp	mRNA	linear	PR1 03-OCT-2003
BC012368	BC012368	Homo sapiens angiopoietin-like 2, IMAGE:5865062, complete cds.				
ACCESSION	BC012368					
VERSION	BC012368.1	GI:15214488				
KEYWORDS	MGC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

REFERENCE	1 (bases 1 to 2178)
AUTHORS	Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Vax, S. I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavani, T. L., Scheer, T. E., Brownstein, M. J., Usdin, T. B., Tostolyaki, S., Grumoli, P., Prange, C., Raha, S. S., Loggiano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., Mccormack, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Wotley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hally, S. W., Viallalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Keltzman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Balesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, R., Myers, R. M., Butcherfield, Y. S., Krzyzinski, M. I., Skalska, U., Smolins, D. E., Suterchak, A., Schein, J. E., Jones, S. J., and Marra, M. A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	22388257
PUBMED	124779932
REFERENCE	2 (bases 1 to 2178)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (15-AUG-2001) National Institutes of Health, Mammalian

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

Email: cga@bcm.tmc.edu
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMI)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Guanaratta, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisgeed, H.,
Gowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Naravati,

A.N., Gibbs, R.A.

Clone distribution MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>

Series: IRAX Plate: 21 Row: k Column: 2

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 612235.

FEATURES

location/Qualifiers

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Source

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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1	Platsky, A., Specht, T., Dahl, E., Hinzmann, B., Rosenthal, A. and		
TITLE	Human nucleic acid sequences of normal uterus tissue		
JOURNAL	Patent: WO 95/94353-A 125-28-OCT-1999;		
	SCHMITT AMMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN		
	BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN		
	(DE); PILARSKY CHRISTIAN (DE)		
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Best Local Similarity	99.3%; Pred. No. 0;		
Matches 2152; Conservative	0; Mismatches 14; Indels 1; Gaps 1;		
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Db	375	AGCCAAACAGAGAGGAAAGAGGCTTTCATTAATTTATATTCACAAAGAAATAACACCATTTT	434
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DEFINITION Human nucleic acid sequence originating in normal uterine tissue.
ACCESSION BD222237
VERSION BD222237.1 GI:33032007
KEYWORDS JP 2002512017-A/66.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3541)
REFERENCE
Specht, T., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and
Rosenthal, A.

TITLE Human nucleic acid sequence originating in normal uterine tissue
JOURNAL Patent: JP 2002512017-A 66 23-APR-2002;
METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
COMMENT OS Homo sapiens (human)
PN JP 2002512017-A/66
PD 23-APR-2002
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PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K38/00, A61P35/00, C07K14/47, C07K16/18,
PC C12N1/19,
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 2152; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
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LOCUS AR081094
DEFINITION Sequence 1 from patent US 5972338.
ACCESSION AR081094
VERSION AR081094.1 GI:10007822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2290)
AUTHORS Godowski, P. J. and Gurney, A. L.
TITLE The ligands homologues
JOURNAL Patent: US 5972338-A 1 26-OCT-1999;
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
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 AUTHORS Godowski,P.J., Guirney,A.L., Hillan,K., Botstein,D., Goddard,A.,
 Roy,M., Ferrera,N., Tunas,D. and Schwalli,R.
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Query Match 98.1%; Score 2132.6; DB 6; Length 2290;
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QY 2103 CTCTTCTTAAATAATTAAGTCTCTTCAATAAAAACA 2141
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LOCUS Sequence 1 from patent US 6586397.
DEFINITION AR350376
ACCESSION AR350376
VERSION AR350376.1 GI:33751435
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2290)
AUTHORS Godowski, P. J. and Gurney, A. L.
TITLES The ligand homologues
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 Ashkenazi, A., Baker, K., Botstein, D., Desnoves, L., Eaton, D. L., Ferrara, N., Fong, S., Gao, W. Q., Gerber, H., Gerlt, M. E., Goddard, A., Godowski, P., Gunney, A., Kijavini, J., Mathew, J., Napper, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C., Williams, P. M., Wood, W. I. and Zhang, Z.
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 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Godowski, P.J., Gurney, A.L., Hillan, K., Botstein, D., Goddard, A.,
Roy, M., Ferrara, N., Tumas, D. and Schwall, R.
Ligand homolog
Patent: JP 2001517437-A 1 09-OCT-2001;
GENENTECH INC

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT
OS Homo sapiens (human)
PN JP 2001517437-A/1
PD 09-OCT-2001
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PAUL J GODOWSKI, AUSTIN L GURNEY, KENNETH HILLAN, DAVID BOTSTEIN, PI
AUDLEY GODDARD, MARGARET ROY, NAPOLEONE FERRARA, DANIEL TUMAS, PI
RALPH SCHWALL
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PC C07K16/18,
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Qy 3 AAATAGAGCTGCTGGAGAGCGGCTGAGAGTGAACCCCAAGCCCTGGAACCTGCGAGAGGTG 62
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2	2132.6	98.1	2290	3	US-09-960-507-1	Sequence 1	Appl1
3	2132.6	98.1	2290	4	US-09-136-828-1	Sequence 1	Appl1
4	2132.6	98.1	2290	4	US-09-332-928A-1	Sequence 1	Appl1
5	2132.6	98.1	2290	4	US-09-136-801-1	Sequence 1	Appl1
6	2132.6	98.1	2290	4	US-09-332-529-1	Sequence 1	Appl1
7	2132.6	98.1	2290	4	US-09-333-075-1	Sequence 1	Appl1
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32	156	7.2	2212	4	US-09-133-801-18	Sequence 18, Appl1
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45	130.4	6.0	1024	3	US-08-934-484-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-933-821-1

Patent No. 5972338

GENERAL INFORMATION

APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L

APPLICANT: Gurney, Aubin L.
TITLE OF INVENTION: Tie ligands

```
NUMBER OF SEQUENCES: 17
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc

STREET: 1 DNA way

CITY: South San Francisco
STATE: CaliforniaSTATE: CALL
COUNTRY: USA

CONTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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;
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,821

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FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
IDENTIFICATION NUMBER: 33

REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:

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; REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-3216

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 2290 base pairs
TYPE: Nucleic Acid

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; TYPE: Nucleic Acid
; STRANDEDNESS: single

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; STRANDEDNESS: single
; TOPOLOGY: Linear

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US-08-933-821-1

100

Query Match	98.1%
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Best. Local Similarity	99.8%
Matches 2135, Conservative	

Matches 2135; conservative

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27

Db 151 AAATGAGGCTGCTGCCGA

[illegible]

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RESULT 2
US-08-960-507-1
; Sequence 1, Application US/08960507
; Patent No. 6057435
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Dregel, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130p1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-960-507-1

Query Match 98.1%; Score 2132.6; DB 3; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 Qy 1743 TACCGAGCGCTTACACAGAGCGAGTCTAATGAGTCTGAGGCTTCCAGAGGCTCTTACTCA 1802
 Db 1891 TACCGAGCGCTTACACAGAGCGAGTCTAATGAGTCTGAGGCTTCCAGAGGCTCTTACTCA 1950
 Qy 1803 CTCAGAGAGTGTATGATGTATCCGACCGAACCCCAACCTTCCATTAAGCCAGCTCC 1862
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 Qy 1863 CCCTCTGACCTCTGTGGCCATTGCGACGAGCCCACTGCTGACGCTGACCAACAGAC 1922
 Db 2011 CCCTCTGACCTCTGTGGCCATTGCGACGAGCCCACTGCTGACGCTGACCAACAGAC 2070
 Qy 1923 AAGAGAACACTCTCTCAACGATTCATCTGAGCTGGAGAGACCGGAGATCTGATCTGT 1982
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 Db 2251 CTCTTCTTAATTAATTAAGTCTCTCAATTAATAA 2289

RESULT 3
 US-09-136-828-1
 Sequence 1, Application US/09136828
 Patent No. 6350450
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,828
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dieger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130R1A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/425-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2290 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single

TOPOLOGY: Linear
 US-09-136-828-1
 Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 AATTAAGCTCTGCTGCGAGCGGCTTGAAGATGAACCCCAAGCCCTGTGACCTGCGGACCTG 62
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 Db 451 AGCCAGCAGAGAGGAGAGGCTTTCATAGATTCATTAACAAGAAATACCAATTT 510
 Qy 363 GCAAAACATGAGGACGACCTGTCGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 422
 Db 511 GCAAGACATGAGGACGACCTGTCGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 570
 Qy 423 GAGCTGTGTGACGAGCGAGAGAGCGTTTGAAGGAGCATGAGAGAGGCTTCCGCAAGAG 482
 Db 571 GAGCTGTGTGACGAGCGAGAGAGCGTTTGAAGGAGCATGAGAGAGGCTTCCGCAAGAG 630
 Qy 483 TTCATTTACTTAACAGATTAACAGCGAGCGGCGAGTCCAGAGACAGTGAACCTACAC 542
 Db 631 TTCATTTACTTAACAGATTAACAGCGAGCGGCGAGTCCAGAGACAGTGAACCTACAC 690
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 Db 691 TTCATTTACTTAACAGATTAACAGCGAGCGGCGAGTCCAGAGACAGTGAACCTACAC 750
 Qy 603 GTCCTTCTGAGAGACGAGTGCATTAAGCAGAGCTGAGCTGCTCAACATGAGCTGCTC 662
 Db 751 GTCCTTCTGAGAGACGAGTGCATTAAGCAGAGCTGAGCTGCTCAACATGAGCTGCTC 810
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 Qy 723 AGCGAGTGAAGCTGCTGCGCAAGAGAGACCCCAATTAATCTCGCGGCTCAAGAGCTTC 782
 Db 871 AGCGAGTGAAGCTGCTGCGCAAGAGAGACCCCAATTAATCTCGCGGCTCAAGAGCTTC 930
 Qy 783 TACATGAGCTCTGACAGAGATCATCCGAAAGCGGCAAGCGCTGTGAGCTCTCCAG 842
 Db 931 TACATGAGCTCTGACAGAGATCATCCGAAAGCGGCAAGCGCTGTGAGCTCTCCAG 990
 Qy 843 CTGAGAGACAGATCTCTGAACAGACAGCCGACATCTGAGCTGCGCAGCAAGTACAG 902
 Db 991 CTGAGAGACAGATCTCTGAACAGACAGCCGACATCTGAGCTGCGCAGCAAGTACAG 1050
 Qy 903 GACCTGAGACAGATTAACAGAGCCTGCGCACTGCGCCACAACTCAAGATCATC 962
 Db 1051 GACCTGAGACAGATTAACAGAGCCTGCGCACTGCGCCACAACTCAAGATCATC 1110
 Qy 963 GCGCAGTTGAGAGACATGCGAGAGGCTGCTGCGGCAAGCGCTTCCCAAGCCACCC 1022

Db 1111 GCGAGCTTGAGAGAGACTGCGAGAGGGGCGCTGCGCAGGCGCGCTGCCAGCACC 1170
 QY 1023 CCGCGTGGCGCGCGCGCGCGCTTACACACACACACACACACACACACACACACAC 1082
 Db 1171 CCGCGTGGCGCGCGCGCGCGCTTACACACACACACACACACACACACACACACAC 1230
 QY 1083 TCTACCAAGAGATCCAGATGAGTACAGACAGACACACACACACACACACACACAC 1142
 Db 1231 TTTACCAAGAGATCCAGATGAGTACAGACACACACACACACACACACACACAC 1290
 QY 1143 ATGCCACTCTTACAGAGCTTCCATCTTCCACACACACACACACACACACACACAC 1202
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 QY 1263 AACACCAACCGCGCTGATGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1322
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 QY 1383 CAAGGCTTGGGAACTTGAAGCGGAGATCTGGGCTGGAGAACATTTACTGGGCTG 1442
 Db 1531 CAAGGCTTGGGAACTTGAAGCGGAGATCTGGGCTGGAGAACATTTACTGGGCTG 1590
 QY 1443 ACGAACCAAGGCACTAACAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1502
 Db 1591 ACGAACCAAGGCACTAACAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1650
 QY 1503 TTTGAGAAATGCGCAGTTTCCGCTGAGAACCTGAGACGAGTATTAATCTGGCTG 1562
 Db 1651 TTTGAGAAATGCGCAGTTTCCGCTGAGAACCTGAGACGAGTATTAATCTGGCTG 1710
 QY 1563 GGGGCGCTACATGAGCAATGCGGCTGCTCTTTCATGATGGCAACCGGCAACAGTTCC 1622
 Db 1711 GGGGCGCTACATGAGCAATGCGGCTGCTCTTTCATGATGGCAACCGGCAACAGTTCC 1770
 QY 1623 ACCCTGAGACAGATCATGATGTCTACACAGAGAACTGTGCCACTTACAGAGAGAGGC 1682
 Db 1771 ACCCTGAGACAGATCATGATGTCTACACAGAGAACTGTGCCACTTACAGAGAGAGGC 1830
 QY 1683 TGGTGTATTAAGCGCTGTGCCCACTCCCAACCTCAACGAGGCTGTGGTACCGGCGGAGCAT 1742
 Db 1831 TGGTGTATTAAGCGCTGTGCCCACTCCCAACCTCAACGAGGCTGTGGTACCGGCGGAGCAT 1890
 QY 1743 TACCGAGACCGCTACAGAGACGAGTCTTACTGGCTGAGTTCCAGAGAGGCTTACTCA 1802
 Db 1891 TACCGAGACCGCTACAGAGACGAGTCTTACTGGCTGAGTTCCAGAGAGGCTTACTCA 1950
 QY 1803 CTCAAGAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
 Db 1951 CTCAAGAAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010
 QY 1863 CCTCTCTGACCTCTGTGTGGCAATGTCAGAGACCCACCTGTGTACAGCTGCGACAGAC 1922
 Db 2011 CCTCTCTGACCTCTGTGTGGCAATGTCAGAGACCCACCTGTGTACAGCTGCGACAGAC 2070
 QY 1923 AAAAGAACTCTCTTCAACAGTTTCACTCTGAGGCTGGAGAGACCGGAGTCTGTGT 1982
 Db 2071 AAAAGAACTCTCTTCAACAGTTTCACTCTGAGGCTGGAGAGACCGGAGTCTGTGT 2130
 QY 1983 TTTCCGAAGTCACTGACAGCGAGTGTGATGATGATGATGATGATGATGATGATGAT 2042
 Db 2131 TTTCCGAAGTCACTGACAGCGAGTGTGATGATGATGATGATGATGATGATGATGAT 2190
 QY 2043 TACTTTCTTCAACAGAGACCGCTCATGTCTTCCAGAGACAGGACAGGACATTAAGACAA 2102
 Db 2191 TACTTTCTTCAACAGAGACCGCTCATGTCTTCCAGAGACAGGACAGGACATTAAGACAA 2250

QY 2103 CTCTTTCTTAAATTAATTAAGTCTCTACATTAATAACA 2141
 Db 2251 CTCTTTCTTAAATTAATTAAGTCTCTACATTAATAAAAA 2289

RESULT 4
 US-09-332-928A-1
 Sequence 1, Application US/09332928A
 Patent No. 6368853
 GENERAL INFORMATION:
 APPLICANT: Godowski, Paul J.
 Gurney, Austin L.
 TITLE OF INVENTION: The Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/332,928A
 FILING DATE: 14-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/933,821
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3215
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2290 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-332-928A-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AAATGAGGCTGCTGCGGAGCGGCTGAGATGAACCCCAAGCCCTGAGACTGCGGAGACTG 62
 Db 151 AAATGAGGCTGCTGCGGAGCGGCTGAGATGAACCCCAAGCCCTGAGACTGCGGAGACTG 210
 QY 63 GCACTGAGGAGCGGCTGACGCTACTGTGAGGAAAGAGTTGTAGCAGGCCCGCAGG 122
 Db 211 GCACTGAGGAGCGGCTGACGCTACTGTGAGGAAAGAGTTGTAGCAGGCCCGCAGG 270
 QY 123 ACCCTGGCGAGCGCTGCGGAGCGGCTGCGGAGCGGCTGTGTGAGGACAGAGTGT 182
 Db 271 ACCCTGGCGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGTGTGAGGACAGAGTGT 330
 QY 183 GAGCCAGTGAAGGAGGAGGCTGTGTGACACCAACCGGCTGCAACTGAGAAACCCCTCAG 242
 Db 331 GAGCCAGTGAAGGAGGAGGCTGTGTGACACCAACCGGCTGCAACTGAGAAACCCCTCAG 390
 QY 243 AGGCTATGACAGAGGCTGCGGCGCTGACGCGCAGGGTGAAGCATGTGAGGACCGGCGCG 302
 Db 391 AGGCTATGACAGAGGCTGCGGCGCTGACGCGCAGGGTGAAGCATGTGAGGACCGGCGCG 450

QY 303 AGCCAGAGAGAGAGAGAGGCTTTTCATAGATTTCTATTCACAAAGATTAACCAACATTTT 362
Db 451 AGCCAGAGAGAGAGAGAGGCTTTTCATAGATTTCTATTCACAAAGATTAACCAACATTTT 510
QY 363 GCAGAGACATAGAGGCACTGTGCTGACATGCTGTGTGCTCGGACTGCTGTGCTGCTGCTG 422
Db 511 GCAGAGACATAGAGGCACTGTGCTGACATGCTGTGTGCTCGGACTGCTGTGCTGCTGCTG 570
QY 423 GGAGCTGTGCAAGGCAAGAGAGAGAGGCTTTTGAAGGCACTGAGAGAGGCTCGCCAGAGAG 482
Db 571 GGAGCTGTGCAAGGCAAGAGAGAGAGGCTTTTGAAGGCACTGAGAGAGGCTCGCCAGAGAG 630
QY 483 TTCAATTTAGCTAAACAGGTATCAAGCGGCGGCGAGTCCAGAGCAATGTGACCTTACACC 542
Db 631 TTCAATTTAGCTAAACAGGTATCAAGCGGCGGCGAGTCCAGAGCAATGTGACCTTACACC 690
QY 543 TTCAATTTAGCTAAACAGGTATCAAGCGGCGGCGAGTCCAGAGCAATGTGACCTTACACC 602
Db 691 TTCAATTTAGCTAAACAGGTATCAAGCGGCGGCGAGTCCAGAGCAATGTGACCTTACACC 750
QY 603 GTGCTTTGAGAGACCGAGTGCATTAAGAGAGAGAGTGTGCTCAACATGAGCTGCTC 662
Db 751 GTGCTTTGAGAGACCGAGTGCATTAAGAGAGAGAGTGTGCTCAACATGAGCTGCTC 810
QY 663 AAGCAGAAAGCGGCAAGATCGAGACGCTGACAGCTGTGAAGGTGAGACGCGGCAATGTG 722
Db 811 AAGCAGAAAGCGGCAAGATCGAGACGCTGACAGCTGTGAAGGTGAGACGCGGCAATGTG 870
QY 723 AAGCAGAAAGCGGCAAGATCGAGACGCTGACAGCTGTGAAGGTGAGACGCGGCAATGTG 782
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QY 1083 TCTACCAACAGATCATCAACAGATCATCAACCGGATCATCAACCGGATCATCAACAGATC 1142
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Db 1291 ATGCCCACTCTCAACAGATCATCAACCGGATCATCAACCGGATCATCAACCGGATCATCAAC 1350
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Db 1351 TGCCTGAGAGGCTTGAAG 1410
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Db 1411 AACACCAACCGGCTTCAAG 1470
QY 1323 GTCATCAAG 1382
Db 1471 GTCATCAAG 1530

QY 1383 CAAGGCTTTGGGAACTTGAACGCGAATATCTGCTGGGCTTGGAGAACTTTACTGCTG 1442
Db 1531 CAAGGCTTTGGGAACTTGAACGCGAATATCTGCTGGGCTTGGAGAACTTTACTGCTG 1590
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Db 1591 ACGAACCAAGGCACTCAAACTCTGTGACATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1650
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Db 1651 TTGCAAGATACGCGCTTCCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1710
QY 1563 GGGCGCTTACATGAG 1622
Db 1711 GGGCGCTTACATGAG 1770
QY 1623 ACCCTGACAGAGATCATGATGCTTACACAGAGAACTGTGCCACTTACAGAGAGAGAGAG 1682
Db 1771 ACCCTGACAGAGATCATGATGCTTACACAGAGAACTGTGCCACTTACAGAGAGAGAGAG 1830
QY 1683 TGTGTGATTAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1742
Db 1831 TGTGTGATTAACGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1890
QY 1743 TACCGAGCGGCTTACAG 1802
Db 1891 TACCGAGCGGCTTACAG 1950
QY 1803 CTCAGAAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1862
Db 1951 CTCAGAAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2010
QY 1863 CCTCTCTGACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1922
Db 2011 CCTCTCTGACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2070
QY 1923 AAGAACCACTCTCTCAACAGATCATCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1982
Db 2071 AAGAACCACTCTCTCAACAGATCATCTGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2130
QY 2043 TACTTCTCTTACACAG 2102
Db 2191 TACTTCTCTTACACAG 2250
QY 2103 CTCTTCTTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2141
Db 2251 CTCTTCTTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2289

RESULT 5
US-09-136-801-1
Sequence 1, Application US/09136801
Patent No. 6413770
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin
APPLICANT: Hillman, Kenneth
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Roy, Margaret
APPLICANT: Ferrara, Napoleone
APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: The Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,801
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/425-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2290 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-09-136-801-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AAATAGGCTGCTGGGAGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 62
 DB 151 AAATAGGCTGCTGGGAGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 210
 QY 63 GCACTGAGGAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 122
 DB 211 GCACTGAGGAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 270
 QY 123 ACCCTGAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 182
 DB 271 ACCCTGAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 330
 QY 183 GAGCCAGTGAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 242
 DB 331 GAGCCAGTGAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 390
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 DB 391 AGGCCATGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 450
 QY 303 AGCCAAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 362
 DB 451 AGCCAAGGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 510
 QY 363 GCAAAAGCAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 422
 DB 511 GCAAAAGCAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 570
 QY 423 GAGAGTGAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 482
 DB 571 GAGAGTGAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 630
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 DB 691 TTCAATTGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 750
 QY 603 GTGCTTGAAGAACGAGTGAACGAGGAGTGAACCCCAAGCCCTGACCTGCTC 662

DB 751 GTGCTTGAAGAACGAGTGAACGAGGAGTGAACCCCAAGCCCTGACCTGCTC 810
 QY 663 AAGCAGAAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 722
 DB 811 AAGCAGAAAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 870
 QY 723 AGCAGAGTGAAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 782
 DB 871 AGCAGAGTGAAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 930
 QY 783 TACATGAGCTCTGAGCAGATATCCGAAAGGAGGAGTGAACCCCAAGCCCTG 842
 DB 931 TACATGAGCTCTGAGCAGATATCCGAAAGGAGGAGTGAACCCCAAGCCCTG 990
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 QY 1143 ATGCCACTCTACACAGCCTCCCATCTTCCACGCAACAGCCCTGCGGAGCTG 1202
 DB 1291 ATGCCACTCTACACAGCCTCCCATCTTCCACGCAACAGCCCTGCGGAGCTG 1350
 QY 1203 TGCTGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1262
 DB 1351 TGCTGAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1410
 QY 1263 AACCAACAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1322
 DB 1411 AACCAACAGGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1470
 QY 1323 GTATCCAGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1382
 DB 1471 GTATCCAGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1530
 QY 1383 CAAGGTTGGGAACTTGAACGAGGAGTGAACCCCAAGCCCTGACCTG 1442
 DB 1531 CAAGGTTGGGAACTTGAACGAGGAGTGAACCCCAAGCCCTGACCTG 1590
 QY 1443 ACBAACCAAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1502
 DB 1591 ACBAACCAAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1650
 QY 1503 TTGAGCAATAGCAGGTTCCGCTGAGAACTGAGAGGAGTGAACCCCAAGCCCTG 1562
 DB 1651 TTGAGCAATAGCAGGTTCCGCTGAGAACTGAGAGGAGTGAACCCCAAGCCCTG 1710
 QY 1563 GGGGCTAACCATGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1622
 DB 1711 GGGGCTAACCATGAGGAGTGAACCCCAAGCCCTGACCTGCGGAGCTG 1770
 QY 1623 ACCCTGAGCAGATATGATGTTCAACAAGAACTGAGGAGTGAACCCCAAGCCCTG 1682
 DB 1771 ACCCTGAGCAGATATGATGTTCAACAAGAACTGAGGAGTGAACCCCAAGCCCTG 1830
 QY 1683 TGGTGTATTAAGCCTGTGCGCACTCAACCTCAAGGAGGAGTGAACCCCAAGCCCTG 1742
 DB 1831 TGGTGTATTAAGCCTGTGCGCACTCAACCTCAAGGAGGAGTGAACCCCAAGCCCTG 1890

QY 1743 TACCGAGCCGCTACAGAGGAGTCTACTGAGTTCGAGAGGCTTTACTCA 1802
DB 1891 TACCGAGCCGCTACAGAGGAGTCTACTGAGTTCGAGAGGCTTTACTCA 1950
QY 1803 CTGAGAGAGTGTATGATGATTCGAGAGGAGTTCGAGAGGCTTTACTCA 1862
DB 1951 CTGAGAGAGTGTATGATGATTCGAGAGGAGTTCGAGAGGCTTTACTCA 2010
QY 1863 CCTCTGAGCTCTGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 1922
DB 2011 CCTCTGAGCTCTGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2070
QY 1923 AAGAGAGAGTGTATGATGATTCGAGAGGAGTTCGAGAGGCTTTACTCA 1982
DB 2071 AAGAGAGAGTGTATGATGATTCGAGAGGAGTTCGAGAGGCTTTACTCA 2130
QY 1983 TTTCCGAGTCTGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2042
DB 2131 TTTCCGAGTCTGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2190
QY 2043 TACTTCTTCAACAGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2102
DB 2191 TACTTCTTCAACAGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2250
QY 2103 CTCTTCTTCAACAGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2141
DB 2251 CTCTTCTTCAACAGAGGAGTTCGAGAGGAGTTCGAGAGGCTTTACTCA 2289

RESULT 6
US-09-332-929-1
Sequence 1, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
US-09-332-929-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 AATGAGGCTGCTGCGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 62
DB 151 AATGAGGCTGCTGCGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 210
QY 63 GCACTGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 122
DB 211 GCACTGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 270
QY 123 ACCCTGCGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 182
DB 271 ACCCTGCGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 330
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DB 391 AGGCTATGAGGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 450
QY 303 AGGCTATGAGGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 362
DB 451 AGGCTATGAGGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 510
QY 363 GCAAGAGCAATGAGGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 422
DB 511 GCAAGAGCAATGAGGAGGCTTGCAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 570
QY 423 GAGCTGTTGCAAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 482
DB 571 GAGCTGTTGCAAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 630
QY 483 TTGATTTAATCTTAAAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 542
DB 631 TTGATTTAATCTTAAAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 690
QY 543 TTGATTTGCTGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 602
DB 691 TTGATTTGCTGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 750
QY 603 GTGCTTCTGAGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 662
DB 751 GTGCTTCTGAGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 810
QY 663 AAGCAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 722
DB 811 AAGCAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 870
QY 723 AAGCAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 782
DB 871 AAGCAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 930
QY 783 TACATGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 842
DB 931 TACATGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 990
QY 843 CTGAGAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 902
DB 991 CTGAGAGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 1050
QY 903 GAGCTGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 962
DB 1051 GAGCTGAGGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 1110
QY 963 GCGAGCTTGAAGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 1022
DB 1111 GCGAGCTTGAAGAGGAGGAGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 1170
QY 1023 CCGGCTGCGGCGGCGGCTTGAAGATGAACTCCAGGCTTGCAGGCTG 1082

[illegible]

	RESULT 7	
	US-09-333-075-1	
	: Sequence 1, Application US/09333075	
	: Patent No. 6492331	
	GENERAL INFORMATION:	
	: APPLICANT: Godowski, Paul J.	
	: APPLICANT: Gurney, Austin L.	
	: TITLE OF INVENTION: Tie Ligands	
	: NUMBER OF SEQUENCES: 17	
	: CORRESPONDENCE ADDRESS:	
	: ADDRESSEE: Genentech, Inc.	
	: STREET: 1 DNA Way	
	: CITY: South San Francisco	
	: STATE: California	
	: COUNTRY: USA	
	: ZIP: 94080	
	COMPUTER READABLE FORM:	
	: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk	
	: COMPUTER: IBM PC compatible	
	: OPERATING SYSTEM: PC-DOS/MS-DOS	
	: SOFTWARE: Winpatin (Genentech)	
	CURRENT APPLICATION DATA:	
	: APPLICATION NUMBER: US/09/333,075	
	: FILING DATE:	
	CLASSIFICATION:	
	: PRIOR APPLICATION DATA:	
	: APPLICATION NUMBER: 08/933,821	
	: FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	: NAME: Dreyer, Ginger R.	
	: REGISTRATION NUMBER: 33,055	
	: REFERENCE/DOCKET NUMBER: P1130	
	TELECOMMUNICATION INFORMATION:	
	: TELEPHONE: 650/225-3216	
	: TELEFAX: 650/952-9881	
	: INFORMATION FOR SEQ ID NO: 1:	
	: SEQUENCE CHARACTERISTICS:	
	: LENGTH: 2290 base pairs	
	: TYPE: Nucleic Acid	
	: STRANDEDNESS: Single	
	: TOPOLOGY: Linear	
	US-09-333-075-1	
	Query Match 98.1%; Score 2132.6; DB 4; Length 2290;	
	Best Local Similarity 99.8%; Pred. No. 0;	
	Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0	
Dy	3 AAATGAGCTCTGCAGCGAAGCCTTGAGGATGAACCCCAAGCCTTGGACTGCCAGCGTG	62
Dd	151 AATGAGGCTCTGTGGAGCGAGCTGAGGATGACCACCAAGCCTTGGACTGCCAGCGTG	210
Dy	63 GCACCTGAGCGAGCGGCTGACGCTACTGTGAGAGAAAGAAGTTGGACAACGCCCGCAGG	122
Dd	211 GCACCTGAGCGAGCGGCTGACGCTACTGTGAGAGAAAGAAGTTGGACAAGCCCCGACGG	270
Dy	123 ACCCTGGCCAGCCCTTGACCCCAAGCCTTCGTGCCGAGACCTCTGTGGAGGACAGGCATG	182
Dd	271 ACCCTGGCCAGCCCTTGACCCCAAGCCTTCGTGCCGAGACCTCTGTGGAGGACAGGCATG	330
Dy	183 GAGCCCATGTGAGCGAGGCTCTTGGCAGGCCAACCGGCTTGAACTCACAGAAACCTCTCAG	242
Dd	331 GAGCCCATGTGAGCGAGGCTCTTGGCAGGCCAACCGGCTTGAACTCACAGAAACCTCTCAG	390
Dy	243 AGGCATGTGACAGGCTGCCCGCTGACGCGCCAGAGGTGAAGCATGTGAGAGAACCGCCCGG	302
Dd	391 AGGCATGTGACAGGCTGCCCGCTGACGCGCCAGAGGTGAAGCATGTGAGAGAACCGCCCGG	450
Dy	303 AGCCAGCAGGAGGAGGAGGCTTTTCATNAGATTCATTTCACAAAGATAACCAACATTTT	362
Dd	451 AGCCAGCAGGAGGAGGAGGCTTTTCATNAGATTCATTTCACAAAGATAACCAACATTTT	510

ORGANISM: Homo Sapiens
US-09-202-088A-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3 AAATGAGGCTGCTGCGAGCGCTGAGTGAACCCCAAGCCCTGAGACTGCGGAGCTG 62
151 AATATGAGCTGCTGCGAGCGCTGAGTGAACCCCAAGCCCTGAGACTGCGGAGCTG 210
63 GCACTGAGGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 122
211 GCACTGAGGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 270
123 ACCCTGAGGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 182
271 ACCCTGAGGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 330
183 GAGCCAGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 242
331 GAGCCAGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 390
243 AGGCGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 302
391 AGGCGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 450
303 AGGCGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 362
451 AGGCGTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 510
363 GCAAGAGCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 422
511 GCAAGAGCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 570
423 GAGGCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 482
571 GAGGCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 630
483 TTCAATTAACCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 542
631 TTCAATTAACCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 690
543 TTCAATTAACCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 602
691 TTCAATTAACCTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 750
603 GTGCTTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 662
751 GTGCTTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 810
663 AAGCAAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 722
811 AAGCAAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 870
723 AAGCAAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 782
871 AAGCAAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 930
783 TACATGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 842
931 TACATGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 990
843 CTGAGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 902
991 CTGAGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 1050
903 GACCTGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 962
1051 GACCTGAGAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 1110
963 GCGGAGCTTGAAGCGGCTGAGCGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 1022

1111 GCGGAGCTTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGCTGAGACTGCGGAGCTG 1170
1023 CCGGCTGAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1082
1171 CCGGCTGAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1230
1083 TCTACAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1142
1231 TCTACAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1290
1143 ATGCGGCTGAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1202
1291 ATGCGGCTGAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1350
1203 TGCGTGAAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1262
1351 TGCGTGAAGAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1410
1263 AACCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1322
1411 AACCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1470
1323 GTCAATCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1382
1471 GTCAATCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1530
1383 CAAGGCTTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1442
1531 CAAGGCTTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1590
1443 ACGAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1502
1591 ACGAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1650
1503 TTGCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1562
1651 TTGCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1710
1563 GGGGCTTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1622
1711 GGGGCTTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1770
1623 ACCCTGAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1682
1771 ACCCTGAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1830
1683 TGGTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1742
1831 TGGTGAAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1890
1743 TACCGAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1802
1891 TACCGAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1950
1803 CTCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1862
1951 CTCAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2010
1863 CCTCTGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1922
2011 CCTCTGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2070
1923 AAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 1982
2071 AAAGAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2130
1983 TTTCAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2042
2131 TTTCAGAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2190
2043 TACTTGAAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2102
2191 TACTTGAAGTGAAGCGGCTGAGCGGCTGAGTGAACCCCAAGCGGCTGAGACTGCGGAGCTG 2250

QY 2103 CTCCTTCTTAATAATTAAGTCTCTACATATAACAA 2141
DB 2251 CTCCTTCTTAATAATTAAGTCTCTACATATAACAA 2289

RESULT 9

US-09-333-077-1
Sequence 1, Application US/09333077
Patent No. 6586397
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-3216
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2290 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-333-077-1

Query Match 98.1%; Score 2132.6; DB 4; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATGAGGCTGCTGGGAGAGGCTGAGATGAACCCCAAGCCCTGAGCTGCGGAGCTG 62
DB 151 AATGAGGCTGCTGGGAGAGGCTGAGATGAACCCCAAGCCCTGAGCTGCGGAGCTG 210
QY 63 GCACTGAGGAGCGGCTGAGCTGCTGAGGAGAAAGAGTTGTGACAGCCCGCAGG 122
DB 211 GCACTGAGGAGCGGCTGAGCTGCTGAGGAGAAAGAGTTGTGACAGCCCGCAGG 270
QY 123 AACCCTGGGCAAGCCCTGCGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGG 182
DB 271 AACCCTGGGCAAGCCCTGCGGAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGG 330
QY 183 GAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 242
DB 331 GAGCCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 390
QY 243 AGGCCATGAGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 302
DB 391 AGGCCATGAGAGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 450

QY 303 AGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 362
DB 451 AGCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 510
QY 363 GCAAGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 422
DB 511 GCAAGACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 570
QY 423 GAGGCTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 482
DB 571 GAGGCTGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 630
QY 483 TTCACTTACCTAAACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 542
DB 631 TTCACTTACCTAAACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 690
QY 543 TTCACTTACCTAAACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 602
DB 691 TTCACTTACCTAAACAGTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 750
QY 603 GTGCTTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 662
DB 751 GTGCTTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 810
QY 663 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
DB 811 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 870
QY 723 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
DB 871 AAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 930
QY 783 TACATCAGAGTCTCTGACAGAGTATCATCCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 842
DB 931 TACATCAGAGTCTCTGACAGAGTATCATCCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 990
QY 843 CTGAGAGAGAGGAGTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 902
DB 991 CTGAGAGAGAGGAGTCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1050
QY 903 GACCTGAGAGCAAGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
DB 1051 GACCTGAGAGCAAGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1110
QY 963 GCGCAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1022
DB 1111 GCGCAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1170
QY 1023 CCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1082
DB 1171 CCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1230
QY 1083 TCTACCAACAGATCCAGAGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1142
DB 1231 TCTACCAACAGATCCAGAGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1290
QY 1143 ATGCCCACTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1202
DB 1291 ATGCCCACTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1350
QY 1203 TGCCTGCAAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1262
DB 1351 TGCCTGCAAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1410
QY 1263 AACACCAACCGGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1322
DB 1411 AACACCAACCGGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1470
QY 1323 GTCATCAAGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1382
DB 1471 GTCATCAAGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1530
QY 1383 CAAGGCTTTGGAGAACATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1442

Db 1308 GGCATTGCGTCAGTGGGATTTATATGATTTAACTGAAAACAGCAATGGACCATGCACT 1367
 Qy 1285 TGTGTGCGACGAGACACGACCCCGGGGCTGAGACCGTCATCCAGAGACCGCTGATG 1344
 Db 1368 TATGTGTGTAACAGTTTGACCTGGGGGTTTGACTGTATTATGAAAAAGAACAGACG 1427
 Qy 1345 GCTCTGTAACTTCTTCAAGAACTGGAGACCTTAAGCAAGGGTTTGGGAACTTGACG 1404
 Db 1428 GCTCTGTAACTTCTTCAAGAACTGGAGAAATTAAGAAAGGTTTGGAAACATTGACG 1487
 Qy 1405 GCGAATTAAGTGGTGGGCTGAGAACATTTACTGGCTGACGAAACCAAGCACTACAAAC 1464
 Db 1488 GAGAAATACGCTGGTGGACCTGAGAAATATCTATATGCTTAAGCAATCAATATTAACAGT 1547
 Qy 1465 TCTGTGTACCAATGAGAGACTGTCCGCGCGAAGTCTTTGCAAAATACCCAGTTCC 1524
 Db 1548 TATTATTAATTAAGACTGAGATTAATAAAAGTCTATGCAAAATACAGCACTTTC 1607
 Qy 1525 GCGTGAACCTGAGACGAGTATTAAGCTGCGCTGGGGGCTACCATGGCAATGCGG 1584
 Db 1608 GCTTGAACCTTAAGTGAATTTCTATTAAGCTGCGCTGGGAACTTACAGGAAATGAG 1667
 Qy 1585 GTGACTCTTTATCATGACCAACGCGCAAGCAAGTTCACCACTTGAACAGATCATGATG 1644
 Db 1668 GCGATTCTATGATGTGGCATTAATGTAACCAATTCACCACTGACAGATTAAGATA 1727
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 Db 1788 ATTCTAACTTAATGAGATGTGTATGAGAGGCGCATTAACGAAAGCAACCAAGATG 1847
 Qy 1765 GAGTCTACTGGGCTAGTTCGAGAGGCTCTTACTCACTCAAGAAATGTGTATGATGA 1824
 Db 1848 GAATTTCTGGGCGCAATACAGAGCGGCTCATCTCTTAAGACAGATTAAGATGATGA 1907
 Qy 1825 TCCGACCGA 1833
 Db 1908 TCAAGCTTA 1916

RESULT 11
 US-08-960-507-3
 / Sequence 3, Application US/08960507
 / Patent No. 6057435
 / GENERAL INFORMATION:
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Garney, Austin L.
 / TITLE OF INVENTION: Tie Ligands
 / NUMBER OF SEQUENCES: 24
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 1 DNA Way
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPatIn (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/960.507
 / FILING DATE:
 / CLASSIFICATION: 536
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Dreger, Ginger R.
 / REGISTRATION NUMBER: 33,055
 / REFERENCE NUMBER: P1130p1
 / TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3355 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-08-960-507-3
 Query Match 22.6%; Score 491.8; DB 3; Length 3355;
 Best Local Similarity 62.9%; Pred. No. 1e-105;
 Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;
 Qy 526 ACAAGTGCACCTTACACTTCATTGTGCTCCAGAGAGGGGTCAAGGGTGCATCTGGTGA 585
 Db 588 AGAAATGTGATACCAATTCCTGTATCTGAACCAAAATTAACAGGCAATCTGTGTGA 647
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 Db 648 ACACCAAGGGGCAAGATGCAAGTACATTAAAGACATGATCAACAGATGAGACTTGAA 707
 Qy 643 TGTCTCAATAGAGTGTCTTCAAGACAGGCGGACATGACAGCTGTGACAGCTGTGA 702
 Db 708 ACTTGAAGAGTGTGCTTCCAGGCAAGCGGAGATGATGTCTTGCACACTGTGTGTG 767
 Qy 703 AGGTGACGGCGGCAATTTGTAGAGAGTGAAGTGTGCGCAAGAGAGAGCCCAATGA 762
 Db 768 ATGTATGTGAACCATTTGTGAATGAGGTAAAGCTGTGAGAAAGGAAAGCCCTTAATGA 827
 Qy 763 ACTCGGGGTCAAGAGCTTCAATGACAGCTCTCTGACAGATCATCCGAACGGGACA 822
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 Qy 823 AGCGGTGAGAGCTCTCCAGCTGAGAGACAGATCTCTGAACAGACAGCGCATGTCTC 882
 Db 888 ATTCACTTGAATCTTCCCACTGGAACCAAAATCTCAATGTCAACACAGAAATGTGA 947
 Qy 883 AGCTGCGACAGATACAGAGACCTGAGACACAGTCCAGACCTGGCCACACTGCGCC 942
 Db 948 AGATGCAACAAAGATACAGGAACTGAGGTGAATAACCTTCTTGAATGATCTTGTGA 1007
 Qy 943 ACAACCAATCAGAGATCTGCGAGCTTGAAGAGATCCAGAGAGGGGCGCTGGGCA 1002
 Db 1008 ATTAACCAATCTGAGATGATCACTTGTGGAAGAACAGTGTGAGATTTTCCGAC 1067
 Qy 1003 GGGCGTCCCGCCAGACCCCGCGTGCCTG-----CCCGGGTCTTACCAACGACCC 1055
 Db 1068 AAGACACCATATGTGTCTCCCGCACTGTGCAAGTGTGCAACAATATCTTAACAGCC 1127
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 Db 1128 AACAGTATCTCTGTGTGCTGGAGGTAAAGAGATTCAGAGGATTCAGGTTATCCCA 1187
 Qy 1116 AAG-----TGCTGCCACCCCTGCTGCCACTATGCGCACTCAACGACCTC-----C 1164
 Db 1188 GAAATTTATGCAACCACTGATGTGCAACTTCTCCCAACCAAAAGCCCTTCAAGATAC 1247
 Qy 1165 CATCTTCAACCGAACCGGTGGGCGCATGAGAGACTGCTGTGAGCGCTGTGAGATG 1224
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 Qy 1285 TGTGTGCGACGAGACACGACCCCGGGGCTGACCGTCAATCAAGAGCGCTGTGATG 1344
 Db 1368 TATGTGTGTAACAGTTTGACCTGGGGGTTGACTGTATTGAGAAAAAGACAGACG 1427
 Qy 1345 GCTCTGTAACTTCTTCAAGAACTGGAGACGTAACAGAAAGGTTTGGGAACTTGAGG 1404
 Db 1428 GCTCTGTCAACTTCTTCAAGAAATGAGAAATTAAGAAAGGTTTGAACATTTGACG 1487

QY 1405 GCGAATCTGCTGGCTGGGAAATTTACTGCTGACGAAACCAAGGCAATCAAAAC 1464
 Db 1488 GAGAAATACGCTTGGACTGGAAATATCTATATGCTTAGCAATCAAGATATATCAAGT 1547
 QY 1465 TCCTGTGACCAATGAGAGACTGTGCGCGCAAGTCTTTGCAAAATACCGCAATTCC 1524
 Db 1548 TATTGATTAATTAAGAGCTGAGAGTATAAAAAGTCTATGCAAAATACAGCACTTTC 1607
 QY 1525 GCTTGAACCTGAGAGCAAGTATTAAGCTGCGCTGCGCGCTACCAATGCAATGCGG 1584
 Db 1608 GCTTGAACCTGAGAGTATTAAGCTGCGCTGCGCGCTACCAATGCAATGCGG 1667
 QY 1565 GTGACTCTCTTATGAGCAACAGGCAAGTCAACCACTGAGCAAGATCATGATG 1644
 Db 1668 GGGATTCTATGATGAGCAATATGATTAAGTAAACATTCACCACTGAGCAAGATTAAGTAT 1727
 QY 1645 TCTACACAGAACTGTGCTCCCACTACCAAGAGAGGCTGTGATTAACGCTGTGCCC 1704
 Db 1728 TGTATGAGGAAATCTGCGCCCACTTCAATTAAGAGGCTGTGATTAAGCTGTGAC 1787
 QY 1705 ACTCAACTCAACGGGCTGTGTATACGGGGGGCCATTAACGGCGCTACCAAGAG 1764
 Db 1788 ATTCTAACCTTAATGAGATATGCTACAGAGAGGCTATTAAGAGCAAGCAACCAAGATG 1847
 QY 1765 GAGTCTAGGCTGAGTTCGAGAGAGGCTCTTACTCACTCAAGAAAGTGTGATGATGA 1824
 Db 1848 GATTTTCTGCGCCCAATACAGAGGCGGCTCATCTCTTAAGAGCAAGTATGATGA 1907
 QY 1825 TCCGACCGA 1833
 Db 1908 TCAAGCTTA 1916

RESULT 12

US-09-136-828-3

Sequence 3, Application US/09136828

Patent No. 6350450

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

TITLE OF INVENTION: The Ligands

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09136,828

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: P113081A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 3355 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Single

TOPOLOGY: Linear

US-09-136-828-3

Query Match 22.6%; Score 491.8; DB 4; Length 3355;
 Best Local Similarity 62.9%; Pred. No. 1e-105;
 Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;

QY 526 ACAAGTACCTTACCTTATGCTGCGGAGAGGCTGACGCTGCTGCA 585
 Db 588 AGAAATGTGATACCACTTCTGCTGACCAAGAAATTAACAGGCGCAATCTGTGCA 647
 QY 586 ACTTCAAGAGCTGAGAGTCTTC--TGAGAACGAGTGCATTAAGAGAGCTAGAGC 642
 Db 648 ACACCAAGGGGCAAGATGCAATGCAATTAAGACATGATCACCAGATGACCTTGAAA 707
 QY 643 TGCTCAACAATGAGTGTCTCAAGCAAGCGGCAATGCAAGCTGCAAGCACTGGTGA 702
 Db 708 ACCTGAAGAGTGTGCTCTCCAGGCAAGCGGAGATAGATGTTCTGCAACTGTGTGG 767
 QY 703 AGGTGACGCGGATTTGTGAGGAGGTGAAGTGTGCGCAAGAGAGCGGCAATGA 762
 Db 768 ATGTAGATGAAACATTTGTGAATGAGGTAAAGCTGTGAAAGAGAAAGCGTTACATGA 827
 QY 763 ACTGCGGGTACGCAAGCTCTACATGCAAGCTCTGCAAGATCATCCGACGGGAGA 822
 Db 828 ACTCTGCTTACTCACTCTATATGCAATTAATTAATGATGATTAATCCGTAAGAGGATA 887
 QY 823 ACCGTTGAGCTCTCCCACTGAGAAACAGATCTGAAACCAAGACGCAATGCTGC 882
 Db 888 ATTCACTTGAATTTCCCACTGAGAAACAAATCTCAATGTCAACCAAGAAATGTGA 947
 QY 883 AGCTGCGCAGCAAGTCAAGAGCCTGAGAGCAAGTACAGCACTGCGCACACTGAGCC 942
 Db 948 AGATGGGAAACAAATACAGGAGACTGAGGTGAATACGCTTCTGATGATCTGTGA 1007
 QY 943 ACAACCAATCAAGATCATGCGGAGCTTGAGAGCACTGCGAGAGGTGCTCGGCA 1002
 Db 1008 ATTAACCAATCTGATGATCATCTTTGTGAAGAACAGTGTGAGAGATATTTTCCGAC 1067
 QY 1003 GGGCGGTCCCGCAGGACCCCGCTGCGCGG-----CCCGGGTCAACCAAGACCC 1055
 Db 1068 AAGACACCATGTGTCTCCCACTGTGCAAGGTGTGCAACATATCTTAAGAGCC 1127
 QY 1056 ACCTACCAACCGATCATCAACAGATCTTACCAAGAGATCCAGAGTACCAAGACTG 1115
 Db 1128 AACAGTATCTCTGTCTGTGAGGATGACAGATTAAGAGGATTCAGGTTATCCCA 1187
 QY 1116 AAG-----TGCTGCAACCCCTGTGCGCACTATGCGCACTCTACAGACTC-----C 1164
 Db 1188 GAGATTTAATGCAACCACTGATCTGCAACTTCTCCCAACAAACCCCTTCAAGATAC 1247
 QY 1165 CATCTTCAACCAAGCGCTGCGGCGCATGAGAGACTGCTGAGAGCGCTGAGATG 1224
 Db 1248 CACCGGAACTTTCAACATGAAGACCAATTAAGACATGTAAGCAAGCAAGAAAGAGCTG 1307
 QY 1225 GCGACAGACAGCTCATCTACCTGTGAGGCGGAGAACCAACCGCTCATGAG 1284
 Db 1308 GGGATTGCTCACTGGGATTTATATTAACCTTAACAGCAATGACCAATGCAAT 1367
 QY 1285 TGTGTGCGACAGAGACAGACCCCGGGGCTGAGCGCTGATCCAGAGAGCGCTGATG 1344
 Db 1368 TATGTGTGAAAACATTTGAGACCTGCGGCTGTGACTTTATTCGAAAAGACAGAG 1427
 QY 1345 GCTCTGTAACTTTCTAGGAACTGGGAGACGTACCAAGAGGTTTGGAAACATTTAGC 1404
 Db 1428 GCTCTGTCAACTTTCAAGAAATTTGGGAAATTAATTAAGAAAGGTTTGGAAACATTTAGC 1487
 QY 1405 GCGAATACGCTGCGGCTGAGGAACTTTACCTGCTGCGAAGCAAGCACTACAAAC 1464
 Db 1488 GAGAAATACGCTTGTGAGCTGGAATATCTATATGCTTGAAGATTAATTAAGAT 1547
 QY 1465 TCCTGTGACCAATGAGAGCTGTGCGCGCAAGTCTTTGCAAAATACCGCAATTCC 1524
 Db 1548 TATTGATTAATTAAGAGCTGAGAGTATAAAAAGTCTATGCAAAATACAGCACTTTC 1607

QY 1525 GCTGGAACCTGAGAGCGAGTATTATTAAGCTGCGGCTGGGGGCTTACCATGGAATGCGG 1584
 Db 1608 GTCTGGAACCTGGAAGTATTATTAAGCTGCGGCTGGGAACTTACCGAGAAATGCGAG 1667
 QY 1555 GTGACTCTTTACATGAGCAACGCGAAGCTTACCACTCTGGAAGAGATCATGATG 1644
 Db 1668 GGGATTCTATGATGATGCGATATGATGAAACATTCACACCTGACAGAGATTAAGATA 1727
 QY 1645 TCTACAGAGAACTGTGCCCACTACAGAGAGAGGCTGTGTATTAACGCTGTGCC 1704
 Db 1728 TGTATGACGAGAACTGCCCACTTCTATTAAGAGAGGCTGTGTATTAAGCTGTGCAC 1787
 QY 1705 ACTCCACCTCAACGCGGCTGTGTATTCGCGGCGGCTTACCGAGCGCTGACAGAGC 1764
 Db 1788 ATTCTAACCTTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1847
 QY 1765 GAGTCTACGAGGCTGAGTTCGAGAGAGGCTCTTACTCACTCAAGAAAGTGTATGATGA 1824
 Db 1848 GAAATTTCTGGGCCCAATACAGAGGCGGCTCACTCTTAAAGACAGTTCAGATGATGA 1907
 QY 1825 TCCGACCGA 1833
 Db 1908 TCAAGCTTA 1916

RESULT 13

US-09-332-928A-3
 Sequence 3, Application US/09332928A
 Patent No. 6368853

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
 TITLE OF INVENTION: Tie Ligands
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIA TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/332,928A
 FILING DATE: 14-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/933,821
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3355 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-332-928A-3
 Query Match 22.6%; Score 491.8; DB 4; Length 3355;
 Best Local Similarity 62.9%; Pred. No. 1e-105;
 Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;

QY 526 ACAAGTCACTTACACCTTCACTTGTGCCCCAGACAGGCGGTACCGGTGCCATCTGCCCTCA 585
 Db 588 AGAAATGTGCAATACATCTTCCGTGACTGTAACAAAGAAATTAACAGGCGCAATCTGTGTCA 647
 QY 586 ACTCCAAAGAGCGCTGAGGCTTCC--TGAGAAACCGAGTGCATTAAGCAGAGAGCTAGAGC 642
 Db 648 AACACAGGCGCAAGATGCAATGCAATACCATTAAGATATATCAACAGATGAGACCTTGAAA 707
 QY 643 TCGTCAACATGAGTGTCTCAAGAGAAACGCGCAGATGAGACGCTGCAAGAGCTGTGTA 702
 Db 708 ACTGMAAGATGTGCTCTCCAGGCAAGACCGGGAATGATGTTCTGCACTGTGGTGTG 767
 QY 703 AGGTGAGCGGCGCAATTGTGAGCGGAGTGAAGCTCTCGCAAGAGAGCGCAACATGA 762
 Db 768 ATGTATGATGAAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 827
 QY 763 ACTCGGCGTCAACGAGCTTATCATGACGCTCTGACAGATCATCCGCAACGCGGCA 822
 Db 828 ACTCTGTGTATCTCACTCTATATGCAATTTATCATGAGATTTATCCGTAAAGGGGATA 887
 QY 823 AGCGTTGAGCTTCTCCAGCTGAGAAACAGATCTGTATACCAACGACAGCGCATGTGCG 882
 Db 888 ATTCACCTTGAACCTTCCCACTGGAACAAATCTCAATGTCCACAGAAATGTTGA 947
 QY 883 AGCTGCGCAGAGTACAAAGACCTGAGCAACAGTACAGCAGCCTGGCCACACTGGCC 942
 Db 948 AGATGCGCAACAGATACAGGGAACCTAGAGGTGAATAGCGCTTCTTGACTGTGTGCA 1007
 QY 943 ACAACCAATGAGATATGCGCAGCTTGTAGAGACACTGCCAGAGGCTGCTTGGGCA 1002
 Db 1008 ATAAACCAATGTGTATGATCACTTTGTGGAAGAACAGTCTTGAAGATATTTTCCGAC 1067
 QY 1003 GGGCGGTCCCGCAGCCACCCCGCTGCGCCG-----CCCGGGGTATCAACACACC 1055
 Db 1068 AAGACACCATGTGTCTCCCACTGTTCAGAGGTGTCACAAATATTCCTTAACAGCC 1127
 QY 1056 ACCTACACCGCATCATCAACAGATCTTCAACAAAGATCAAGATGACCAAGAACTG 1115
 Db 1128 AACAGATATCTCTGTGTGTGAGAGGTAAAGAAATTCAGAGGATCCAGGTATCCCA 1187
 QY 1116 AAGG-----TGCAGCACCCCGCTGCGCCACTGATGCGCCACTCTCAACAGCTC-----C 1164
 Db 1188 GAAATTAATGACACACCTGATCTGGAACCTTCTCCACCAAAAGCCCTTCAAGATAC 1247
 QY 1165 CATCTTCAACGCAACAGCGGTGCGGCAATGAGAGACTGCTGAGGCGCTTGAAGATG 1224
 Db 1248 CACCGGTAACTTTCATCATGATGAGAGCAATCAAGACTGTGACAGCAAGCAAGAAAGCTG 1307
 QY 1225 GCGACACACAGCTCCATCTACCTGTGTAAGCCGGAAGAACCAACGCGCTCATGCAAG 1284
 Db 1308 GGCATTCGCTCAGTGGGATTTATGATTTAACTGAAACAGCAATGACCAATGCACT 1367
 QY 1285 TGTGTGCGACAGAGACAGACAGACCCCGGGGCTGACCGCTCATCAAGACGCTGAGT 1344
 Db 1368 TATGTGTGAAAACAGTTTGAACCTGCGGGTTGACCTGTTATTCGAAAAGAACAGACG 1427
 QY 1345 GCTGTGTTAACTTCTTCAAGAACTGGGAGACGTACAGCAAGGTTTGGGAACATTGACG 1404
 Db 1428 GCTGTGTCAACTTCTTCAAGAAATTTGGGAAATTTAAAGAAAGGTTTGGAAACATTGACG 1487
 QY 1405 GCGAATACGCGCTGGGCTGAGAACTTATGCTGCTGCAAGCAAGGCAACTACAAAC 1464
 Db 1488 GAGAAATACGCTTGGACTGGAATAATCTATATGTGTGCAATGAAATATTAACAAGT 1547
 QY 1465 TCTGTGTGACATGAGAGACTGTGCGCGGCAAAAGCTTTGCAAGATAGCCAGTTTCC 1524
 Db 1548 TATTGATTGAATTAGAAAGCTGAGATGATTAAGAAAGTCTATGCAAGATGCAAGCTTTC 1607
 QY 1525 GCTGGAACCTGAGACGAGTATTATTAACCTGCGCTGGGGGCTACCATGCAATGCGG 1584
 Db 1608 GTCTGGAACCTGGAAGTATTAATGACTGCGCTGGAACTTACCGAGAAATGCGAG 1667
 QY 1585 GTGACTCTTTACATGAGCAACGCGCAAGAGCTTACCACTTGAACAGATCATGATG 1644

Db 1668 GGGATTCTATGATGTGGCATTAATGTAACCAATTACCACTGAGACAGATTAAGATA 1727
 Qy 1645 TCTACACAGAAACTGTGCTCCACTACAGAGAGAGGCTGTGTATTAAGCTTGTGCC 1704
 Db 1728 TGTATGACAGAACTGCGCCACTTTCATTAAGAGAGGCTGTGTATTAAGCTTGTGAC 1787
 Qy 1705 ACTCCAACTCAACGAGGCTGTGTACCGGCGGCGCATTAACGAGCGCTTACAGAGC 1764
 Db 1788 ATTCTAATTAATGAGATGATGTACAGAGAGCGCATTAACAGACCAAGCATG 1847
 Qy 1765 GAGTCTACTGAGCTGATGTCGAGAGAGCTCTTACTCACTCAAGAAAGTGTGATGATGA 1824
 Db 1848 GAATTTTCTGCGGCGCAATACAGAGGCGGTCTACTCTTAAGAGCAGTTGATGATGA 1907
 Qy 1825 TCCGACCGA 1833
 Db 1908 TCAAGCTTA 1916

RESULT 14

US-09-136-801-3
 ; Sequence 3, Application US/09136801
 ; Patent No. 6413770

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Botstein, David
 APPLICANT: Goddard, Audrey
 APPLICANT: Roy, Margaret
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Tumas, Daniel
 APPLICANT: Schwall, Ralph
 TITLE OF INVENTION: Tie Ligand Homologues
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/136,801
 FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Ginger R.
 REGISTRATION NUMBER: 33,055
 REFERENCE/DOCKET NUMBER: P1130P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-3216
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3355 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-09-136-801-3

Query Match 22.6%; Score 491.8; DB 4; Length 3355;
 Best Local Similarity 62.9%; Pred. No. 1e-105;
 Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;

Qy 526 ACAATGCACTTCACTTCACTTGTGCCCCAGACGGGCTCAGGGGCTCATCTGCTCA 585

Db 588 AGAATGTGATACATCATCTCTGTACTGAAACAAAGATTAACAGGGCAATCTGTCTCA 647
 Qy 586 ACTCCAAAGAGCTGAGTGTCTC---TGAAGAACCAAGTGCATTAAGACAGTACAGC 642
 Db 648 ACACCAAGGGGCAAGAGCAAGTACCAATTAAGACATGATCACAGATGAGACCTTGAAA 707
 Qy 643 TGCTCAACATGAGCTCTCTCAAGAGAGGAGAGTCAAGCTGAGAGCTGAGAGCTGAGTGA 702
 Db 708 ACTGAAAGATGTCTCTCTCAAGCAGAGCGGAGATGATGTCTGCAACTGTGTGG 767
 Qy 703 AGGTGACGCGGCAATTTGTAGCGAGGTGAGCTGTGCGCAAGAGAGCGCAACATGA 762
 Db 768 ATGTAGATGAAACATTTGTAATGAGGTAAAGCTGTGAGAAAGAGCGCTTAACATGA 827
 Qy 763 ACTGGGGGTCAAGCACTCTAATGAGTCTCTGCAAGAGATCATTCGGAACCGGGACA 822
 Db 828 ACTCTGTGTACTCAACTCTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 887
 Qy 823 ACGGTTGAGCTCTCTCCAGCTGAGAAACAGATCTTGAACCAAGACCGCAATGCTGC 882
 Db 888 ATTCACTTGAACCTTCCCACTGGAACCAAAATTCCTCAATGTCAACCAAGAAATGTGA 947
 Qy 883 AGCTGGCCAGCAAGTAAAGAACTGTGAGCAAGTACAGACCTGTGCCACTGTGCC 942
 Db 948 AGATGGCAACAAATACAGGAACTGAGGTGAATACGCTTCTTGAATGATCTGTCA 1007
 Qy 943 ACAACCAATCAGAGATCATGCGCAGCTTGAAGAGCACTGCAAGAGGTGCTCGGCCA 1002
 Db 1008 ATACCAATCTGTGATATATCACTTTGTGAAAGACAGTCTTGAGATATTTTCCGAC 1067
 Qy 1003 GGGCCGTCCCAAGCAACCCCGCTGCCCCG-----CCCGGGTCTTCAACCAACC 1055
 Db 1068 AAGCAACCCATGTGTCTCCCACTTGTCCAGGTGTGCAACCAATATCTTAACAGCC 1127
 Qy 1056 ACCACAGAGCAATCAACCAAGATCTTACCAAGATCCAGATGACCAAGACTG 1115
 Db 1128 AACGATATCTCTGT 1187
 Qy 1116 AAGG-----TGCTGCCAACCCTCTGCCCCACTATGCCCCACTTACACAGCTC-----C 1164
 Db 1188 GAGATTTAATGCCACCACTGATCTGCAACTTCTCCACCAAAAGCCCTTCAAGATAC 1247
 Qy 1165 CATCTTCCACCAAGACCGCTGCGGCCCATGAGAGATCTGCTGAGGCGCTGAGAGAT 1224
 Db 1248 CACCGTAACTTTATCAATGAAGAACCAATTAACCTGTGCAAGCAAAAGAGCTG 1307
 Qy 1225 GCCACGACACCACTCATCTACCTGTGAAGCGGAGAACCAACCGCTCATGAGG 1284
 Db 1308 GGCATTCGTCACATGGGATTTATATGATTAACCTGAAACAGCAATGACCAATGCAGT 1367
 Qy 1285 TGTGTGCGACCAAGACGACCGCCGGGGCTGACCGTATCCAGAGCGCTGAGATG 1344
 Db 1368 TATGTGTGAAACAGTTTGAACCTGCGGGGTGACCTGTATTCAGAAAGAACAGAG 1427
 Qy 1345 GCTCTGTAACTCTTCAAGAACTGGAAGCGTACAGAGAGGCTTGGAAACATGAGG 1404
 Db 1428 GCTCTGTCACTCTTCAAGAACTTGGAAATTAATTAAGAAAGGCTTGGAAACATGAGG 1487
 Qy 1405 GCGAATACGTGCTGAGCTTGAACATTTACTGTGTCGAAACCAAGCAATCAACAA 1464
 Db 1488 GAGAAATACGTGCTGAGCTGAAATATCTATGTGCTTGAATCAAGATTAATCAAGT 1547
 Qy 1465 TCCGTGAGCAATGAGAGAGCTGTGCGGCCGCAAAATCTTTGAGAAATGCGAGTTGCC 1524
 Db 1548 TATTGATGATTTAGAACTGAGTGAATTAAGAAAGCTTATGAGATACAGACCTTTC 1607
 Qy 1525 GCGTGAACCTGAGACGAGATTTATTAAGCTGCGGCTGAGGCGCTTCAATGCAATGCGG 1584
 Db 1608 GTCTGGAACCTGAAAGATTTATTAAGCTGCGGCTGAGGAACTTCAAGGGAATGAGG 1667
 Qy 1585 GTGACTCTTTATCATGAGCAACGCAAGCAAGTTCACACCTTGTGACAGAGATCATGATG 1644
 Db 1668 GGGATTCTATGATGTGCAATTAATGTAACCAATTCACCACTGACAGAGATTAAGATA 1727

1645 TCTACACGAACTGTGCTCCACCTACGAGAGAGGCTGTGTATTAAGCCCTGTGCCC 1704
1728 TGTATGACGAGAACTGCGCCCACTTCTAATAAGAGAGCTGTGTATTAAGCTGTGAC 1787
1705 ACTCCAACTCAACCGGCTGTGTATCCGCGGCGCATTAACGAGCCGCTACAGAGAG 1764
1788 ATTCTAACCTTAATGAGATATGTATCAAGAGAGGCAATTAAGAGAGAGAGAGATG 1847
1765 GAGTCTACTGCGCTGAGTTCGAGAGAGGCTTCTACTACTCAAGAAAGTGTATGATGA 1824
1848 GAATTTCTGGGCGCCGATACAGAGCGGCTACTCTTAAAGACAGTTCAGATGATGA 1907
1825 TCCGACCGA 1833
1908 TCAAGCTTA 1916

RESULT 15

US-09-332-929-3
Sequence 3, Application US/09332929
Patent No. 6420542
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/332,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/933,821
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dregar, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1130
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-09-332-929-3

Query Match 22.6%; Score 491.8; DB 4; Length 3355;
Best Local Similarity 62.9%; Pred. No. 1e-105;
Matches 836; Conservative 0; Mismatches 472; Indels 21; Gaps 4;

DB 526 ACAAGTACCTACACCTTATGTCGCCACAGCGGGTCAAGGGTCCATCTGCGTCA 585
DB 588 AGAAATGTGATACATCTCTGTATCTGAAACAAGATTAACAAGGCGCAATCTGTGTCA 647
QY 586 ACTCCAGAGAGCTGAGTGTTC---TGGAGAACGAGTGCATTAAGAGAGAGCTAGAGC 642
DB 648 ACACCAAGGAGAGATGCAAGTACCATTAAGACATGATCACCGAGATGACCTTGAAA 707

QY 643 TGTCAACAAATGAGTGTCTCAAGAGAAAGCGAGATGAGACGCTGACAGACTGTGTA 702
DB 708 ACTGAGAGATGTGCTCTCAGGACAGAGCGGAGATATGATGTTCTGCAACTGTGTGTG 767
QY 703 AGGTGAGCGCGGCATTGTGAGCGAGTGAAGTCTCTCGCAAGAGAGCGGCACATGA 762
DB 768 ATGTAGATGAAACATGTGAATGAGTGAACCTCTGAGAAAGAGAGCGGTAACTAGA 827
QY 763 ACTGCGGCTGACGAGCTCTACATGACAGCTCTGACAGATCAATCCGCAAGCGGACA 822
DB 828 ACTCTGCTGTACTCACTCTATATGCAATTTATACATGAGATTTATCCGTAAAGAGATA 887
QY 823 AGCGTTGAGCTCTCCAGCTGAGAGAACAGATCTTGAACCAAGACAGCCGATGCTGC 882
DB 888 ATCACTTGAATCTTCCCACTGAGAAACAAATCTCTCAATGTCAACAGAAATGTGA 947
QY 883 AGCTGCGCAGCAAGTACAGAGACTGAGAGCAAGATACAGACCTGCGCACTGCGCC 942
DB 948 AGATGCAACAAAGATACAGAGAACTTAGAGTGAATACCTCTCTGATGATCTGTGCA 1007
QY 943 ACAACCAATCAGAGATCATGCGCAGCTTGAGAGCACTGCAAGAGGTCCTTGAGCCA 1002
DB 1008 ATACCAATCTGATGATCATCTTGTGAGAAACAAGTGTGAGGATATTTTCCGAC 1067
QY 1003 GCGCCGTCGCCAGACCCCGCGCTGCGCCG-----CCCGGGTCTAACCAACACCC 1055
DB 1068 AAGACACCATGTGTCTCCCACTGTTCAGAGTGTGCAACAATATCTTCAAGAGC 1127
QY 1056 ACCTACACCGCATCATCAACCAAGATCTTACCAAGAGATCAGAGTACCAAGACTG 1115
DB 1128 AACAGATATCTCTGTGTGTGAGAGTAAAGATTCAGAGGATCCAGGTATTCCTCA 1187
QY 1116 AAGG-----TGTGCGCAACCCCTCTGCGCACTATGCGCATCTGCACAGCCCTC-----C 1164
DB 1188 GAATTTAATGCGACACCACTGATCTGCAACTCTCCCAACAAAGCCCTTCAAGATAC 1247
QY 1165 CATCTTCAACCGACAGAGCGCTGCGCCATGAGAGACTGCTGAGAGCGCTGAGAGATG 1224
DB 1248 CACCGGTAATCTTCAATCAATGAAGACACTTGAAGACTGTGAGAGAGAAAGAGCTG 1307
QY 1225 GCCACGACACCACTTCATCTACTGTGTAAGCGGAGAACCAACCGCTCATAGCAG 1284
DB 1308 GGCATTCGGTCAAGTGGAGTTATATGATTAACCTGAAACAGCAATGACCAATGACGT 1367
QY 1285 TGTGTGCGACACAGACAGACCGCGGGGCTGAGCGCTCATGACAGAGCGCTGATG 1344
DB 1368 TATGTGTGAAACAGCTTTGACCTTGGGGTGTGACTGTATTGAGAAAGAACAGAG 1427
QY 1345 GCTCTGTAACTTCTTCAAGAACTGAGACGTACAGCAAGCGTTTGGAACTTTGACG 1404
DB 1428 GCTCTGTCAACTCTTCAAGAAATGGAATAATTAAGAAAGGTTTGGAAACATTTAG 1487
QY 1405 GCGAATATCTGCTGGGCTGAGAAACATTTACTGCTGACGAAACCAAGGCACTTCAAC 1464
DB 1488 GAGAAATACGCTTGAAGTGAATAATCTATATGTGTGCAATCAAGTAATTTACAGT 1547
QY 1465 TCTGTGTACCATGAGAGACTGTGCGCGGCAAGTCTTTGAGAAATGAGCAATTTTC 1524
DB 1548 TATTGATGATTAAGAACTGAGTGAATAAAGTCTATGAGAAATCAGACGCTTTC 1607
QY 1525 GCTGGAACCTGAGAGCGAGTATTAAGCTGTGCGGCTGAGGCGCTTACCTATGCAATGCG 1584
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QY 1705 ACTCCAACTCAACCGGCTGTGTATCCGCGGCGCATTAACGAGCCGCTACAGAGAG 1764

Mon Aug 9 10:30:08 2004

us-10-018-386-1.rni

Page 19

Db	1788	ATTCTAACCTAATGAGATGTGTACAGAGGAGCCATTACAGAAACCAAGCACCAAGATG	1847
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Search completed: August 6, 2004, 18:18:56
Job time : 172 secs

/ APPLICANT: Desnyers, Luc
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Sherwood, Steven
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Matanabe, Colin K
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / FILE REFERENCE: P330R1C345
 / CURRENT APPLICATION NUMBER: US/10/147,493
 / CURRENT FILING DATE: 2002-05-17
 / Prior Application removed - See File Wrapper or Palm
 / NUMBER OF SEQ ID NOS: 550
 / SEQ ID NO 267
 / LENGTH: 2290
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / US-10-147-493-267

Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 QY 63 GCACTGAGGACGCGCTGACGCTACTGTGAGGAAAGAGTTGTGAGAGCCCGCAGAG 122
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 QY 123 ACCCTGCGGACGCGCTGCGCCCAAGCTTCTGCGGAGCCCTCTGTGAGGACGCGCAGT 182
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 QY 243 AGGCGATGAGACGCGCTGCGCCCAAGCTTCTGCGGAGCCCTCTGTGAGGAGCCCGCAG 302
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 DB 511 GCAAGACCATGAGGACGCTGCGTGAATGCTGTGAGGAGGCTGCGCAGTGCATG 570
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QY 1743 TACCGAGCCGCTACGAGAGAGTCTAGTTCGAGAGGCTCTTACTGA 1802
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 Db 2191 TACTTCTCTGACGAG 2250
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 / Sequence 267, Application US/10145127
 / Publication No. US20040033558A1
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Beresini, Maureen
 / APPLICANT: Deforge, Laura
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gutney, Austin L.
 / APPLICANT: Sherwood, Steven
 / APPLICANT: Smith, Victoria
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watanabe, Colin K
 / APPLICANT: Wood, William
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / FILE OF INVENTION: ACIDS ENCODING THE SAME
 / FILE REFERENCE: P330R1C252
 / CURRENT APPLICATION NUMBER: US/10/145,127
 / PRIORITY FILING DATE: 2002-05-13
 / PRIORITY APPLICATION REMOVED - See File Wrapper or Palm
 / NUMBER OF SEQ ID NOS: 550
 / SEQ ID NO 267
 / LENGTH: 2290
 / TYPE: DNA
 / ORGANISM: Homo Sapien
 / US-10-145-127-267

Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
 Best Local Similarity 99.8%; P-adj. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 AAATGAGCTGCTGCGAGAGGCTTGAAGATGAACCCCAAGCCCTGAGCTGCGAGCTG 62
 Db 151 AAATGAGCTGCTGCGAGAGGCTTGAAGATGAACCCCAAGCCCTGAGCTGCGAGCTG 210

QY 63 GCACTGAGGAGGAGCTGAGAGCTACTGTGAGGAGAAAGAGTTGTGAGAGGCCCCGAGAG 122
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 QY 123 ACCCTTGGCCAGCCCTGAGGCTGAGCTTGTGAGAGGCTTGTGAGAGGAGGAGGAGG 182
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 QY 183 GAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
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Mon Aug 9 10:30:08 2004

us-10-018-386-1.rnpb

Page 5

Dp	1291	ATGCCCACTCTACCAAGCTCCCATCTTCCACCGACAAAGCGCTCGGGCCCATGGAGAGAC	1350
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RESULT 4
US-10-160-503-267
; Sequence 267, Application US/10160503
; Publication No. US20040033552A1
; GENERAL INFORMATION:

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? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Maureen
? APPLICANT: DeForge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Gerritsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? TITLE OF INVENTION: ACIDS ENCODING THE SAME
? FILE REFERENCE: P3350R1C446
? CURRENT APPLICATION NUMBER: US/10/160,503
? CURRENT FILING DATE: 2002-05-30
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 267
? LENGTH: 2290
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-160-503-267

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Best Local Similarity	99.8%	Pred. No. 0		
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Db 991 CTGGAAGAAAGATCTCTGAACAGACGCGCATGCTGAGCTGTGCGCAGCAAGTACAAG 1050
QY 903 GACCTGAGACCAAGTACCAAGCACTGTGAGCACTGTGAGCCCAACCAATCAAGATCATC 962
Db 1051 GACCTGAGACCAAGTACCAAGCACTGTGAGCACTGTGAGCCCAACCAATCAAGATCATC 1110
QY 963 GCGCACTTGAAGAGCTGTGAGAGGAGTGTGCTGTGAGAGGCGCTGTGAGAGGCGCAGC 1022
Db 1111 GCGCACTTGAAGAGCTGTGAGAGGAGTGTGCTGTGAGAGGCGCTGTGAGAGGCGCAGC 1170
QY 1023 CCGGCTGCGCGCGCGGCTGTACCAACCAAGCTGTGAGAGGCGCTGTGAGAGGCGCAGC 1082
Db 1171 CCGGCTGCGCGCGCGGCTGTACCAACCAAGCTGTGAGAGGCGCTGTGAGAGGCGCAGC 1230
QY 1083 TTACCAAGAGAGTCCAGAGTGAAGAGGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 1142
Db 1231 TTACCAAGAGAGTCCAGAGTGAAGAGGAGGCTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 1290

QY 1143 ATGCCCACTCTACCAAGCTTCCATCTTTCACCAAGAGCCGTGAGGCGCCATGAGAGAC 1202
Db 1291 ATGCCCACTCTACCAAGCTTCCATCTTTCACCAAGAGCCGTGAGGCGCCATGAGAGAC 1350
QY 1203 TGCTGTGAGGCGCTGTGAGAGTGTGCAAGCACTGTGAGCTGTGAGAGCTGTGAGAG 1262
Db 1351 TGCTGTGAGGCGCTGTGAGAGTGTGCAAGCACTGTGAGCTGTGAGAGCTGTGAGAG 1410
QY 1263 AAGCAACAGCGCTGTGAGAGTGTGCAAGCACTGTGAGCTGTGAGAGCTGTGAGAG 1322
Db 1411 AAGCAACAGCGCTGTGAGAGTGTGCAAGCACTGTGAGCTGTGAGAGCTGTGAGAG 1470
QY 1323 GTCATCCAGAGAGCGCTGTGAGTGTGTAACCTTTCAGAGAACTGTGAGAGCTGTGAG 1382
Db 1471 GTCATCCAGAGAGCGCTGTGAGTGTGTAACCTTTCAGAGAACTGTGAGAGCTGTGAG 1530
QY 1383 CAAGGTTTGGGAACTTTGACGCGGAGTATCTGTGAGGCGCTGTGAGAACTTTTACG 1442
Db 1531 CAAGGTTTGGGAACTTTGACGCGGAGTATCTGTGAGGCGCTGTGAGAACTTTTACG 1500
QY 1443 ACGAACAAGGCACTACAACTCTGTGTGACATGAGAGAGCTGTGCGGCGCAAGATC 1502
Db 1591 ACGAACAAGGCACTACAACTCTGTGTGACATGAGAGAGCTGTGCGGCGCAAGATC 1560
QY 1503 TTTGCAAAATACGCCAGTTTCCGCTGTGAGACTGTGAGAGCGAGTATTAAGCTGTG 1562
Db 1651 TTTGCAAAATACGCCAGTTTCCGCTGTGAGACTGTGAGAGCGAGTATTAAGCTGTG 1710
QY 1563 GAGGCTTACCATGTGCAATGTGAGGAGTGTGCTTTCATGTGCAAGCAAGGCAAGCTTAC 1622
Db 1711 GAGGCTTACCATGTGCAATGTGAGGAGTGTGCTTTCATGTGCAAGCAAGGCAAGCTTAC 1770
QY 1623 ACCCTGACAGAGATCATGATGTCTACAAGAGAACTGTGCCACTACCAAGAGGAGG 1682
Db 1771 ACCCTGACAGAGATCATGATGTCTACAAGAGAACTGTGCCACTACCAAGAGGAGG 1830
QY 1683 TGTGTGTATTAAGCTGTGAGGCGCACTGTGAGAGGCTGTGAGAGGCTGTGAGAGG 1742
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QY 1743 TACCGAGGCGCTACAGAGAGGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 1802
Db 1891 TACCGAGGCGCTACAGAGAGGAGTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 1950
QY 1803 CTCAAGAAAGTGTGATGATATATCCGACCAAGCCCAACACTTTCACCTAAGCCAGCTCC 1862
Db 1951 CTCAAGAAAGTGTGATGATATATCCGACCAAGCCCAACACTTTCACCTAAGCCAGCTCC 2010
QY 1863 CCTCTGACCTCTGTGAGGCGCTGTGAGAGGCGCACTGTGAGAGGCTGTGAGAGG 1922
Db 2011 CCTCTGACCTCTGTGAGGCGCTGTGAGAGGCGCACTGTGAGAGGCTGTGAGAGG 2070
QY 1923 AAGAAACAACTCTACCAAGTTCATCTGTGAGCTGTGAGAGAGCGGAGTGTGATCTGT 1982
Db 2071 AAGAAACAACTCTACCAAGTTCATCTGTGAGCTGTGAGAGAGCGGAGTGTGATCTGT 2130
QY 1983 TTTCCGAAGTACCTGTGAGGCGGAGTGTGAGAACTGAATGATGATGATGATGATGATG 2042
Db 2131 TTTCCGAAGTACCTGTGAGGCGGAGTGTGAGAACTGAATGATGATGATGATGATGATG 2190
QY 2043 TACTTTCTTCAACCAAGAGAGGCGCTGTGATGTCTTCAAGAGAGAGAGCTACAGCAA 2102
Db 2191 TACTTTCTTCAACCAAGAGAGGCGCTGTGATGTCTTCAAGAGAGAGAGCTACAGCAA 2250
QY 2103 CTCTTTCTTAAATTAATTAATGCTCTTCAATTAATAA 2141
Db 2251 CTCTTTCTTAAATTAATTAATGCTCTTCAATTAATAA 2289

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QY	1663	TGTTGGTATTAACGGCTGTGGCCACTCCAACTCCAAAGGGGTGTGTATCCGCGGGGCCAT	1742
Db	1831	TGTTGGTATTAACGGCTGTGGCCACTCCAACTCCAAAGGGGTGTGTATCCGCGGGGCCAT	1830
QY	1743	TACCGGACCCGGTATCCAGGACGAGATCTACTGGGCTGAGTTCCGAGAGGCTTTACTCA	1802
Db	1891	TACCGGACCCGGTATCCAGGACGAGATCTACTGGGCTGAGTTCCGAGAGGCTTTACTCA	1950
QY	1803	CTCAAGAAAGTGTGTATGTATGCCAGCCGAAACCCCAACCTTCCACTTAAGCCAGCTCC	1862
Db	1951	CTCAAGAAAGTGTGTATGTATGCCAGCCGAAACCCCAACCTTCCACTTAAGCCAGCTCC	2010
QY	1863	CCCTTCCTAACCTCTGTGGCCATTGGCAGGAGGCCACCTGGTACACGTGGCCACAGAC	1922
Db	2011	CCCTTCCTAACCTCTGTGGCCATTGGCAGGAGGCCACCTGGTACACGTGGCCACAGAC	2070
QY	1923	AAAGAACCACTCTTCACCACTTCATCTGAGGCTGGAGGACCGGGAATGCTGATTTCTGT	1982
Db	2071	AAAGAACCACTCTTCACCACTTCATCTGAGGCTGGAGGACCGGGAATGCTGATTTCTGT	2130
QY	1983	TTTCCGAGTCACTGCAAGCCGATGATGGAATCGAATACGGGTGTTTCTGTCCCTCC	2042
Db	2131	TTTCCGAGTCACTGCAAGCCGATGATGGAATCGAATACGGGTGTTTCTGTCCCTCC	2190
QY	2043	TACTTTCCTTCAACACAGACAGCCCTCATGTCTCCAGGACAGGACAGATACAGACAA	2102
Db	2191	TACTTTCCTTCAACACAGACAGCCCTCATGTCTCCAGGACAGGACAGATACAGACAA	2250
QY	2103	CTCTTCTTTAAATTAATTAAGTCTTCACATTAATAACA	2141
Db	2251	CTCTTCTTTAAATTAATTAAGTCTTCACATTAATAAAAA	2289

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RESULT 7
US-10-158-787-267
1 Sequence 267, Application US/10158787
2 Publication No. US20040039164A1
3 GENERAL INFORMATION:
4 APPLICANT: Baker, Kevin P.
5 APPLICANT: Beresini, Maureen
6 APPLICANT: DeForge, Laura
7 APPLICANT: Desnoyers, Luc
8 APPLICANT: Filvaroff, Ellen
9 APPLICANT: Gao, Wei-Qiang
10 APPLICANT: Gerritsen, Mary E.
11 APPLICANT: Goddard, Audrey
12 APPLICANT: Godowski, Paul J.
13 APPLICANT: Gurney, Austin L.
14 APPLICANT: Sherwood, Steven
15 APPLICANT: Smith, Victoria
16 APPLICANT: Stewart, Timothy A.
17 APPLICANT: Tumas, Daniel
18 APPLICANT: Watanabe, Colin K
19 APPLICANT: Wood, William
20 APPLICANT: Zhang, Zemin
21 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
22 FILE REFERENCE: P3330R1C49
23 CURRENT APPLICATION NUMBER: US/10/158,787
24 CURRENT FILING DATE: 2003-04-03
25 PRIOR APPLICATION NUMBER: 60/049911
26 PRIOR FILING DATE: 1997-06-18
27 PRIOR APPLICATION NUMBER: 60/056974
28 PRIOR FILING DATE: 1997-08-26
29 PRIOR APPLICATION NUMBER: 60/059113
30 PRIOR FILING DATE: 1997-09-17
31 PRIOR APPLICATION NUMBER: 60/059115
32 PRIOR FILING DATE: 1997-09-17
33 PRIOR APPLICATION NUMBER: 60/059117
34 PRIOR FILING DATE: 1997-09-17
35 PRIOR APPLICATION NUMBER: 60/059122

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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 267
; LENGTH: 2290
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-158-787-267

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Query Match	98.1%	Score 2132.6	DB 13	Length 2290
Best Local Similarity	99.8%	Pred. No. 0		
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QY	3	AAATGAGGCTCTGTCGAGACGGCTTGAGGANTGAACCCCAAGCCTTGAGACTGCGGAGCGTG	62	
Db	151	AAATGAGGCTCTGTCGAGACGGCTTGAGGANTGAACCCCAAGCCTTGAGACTGCGGAGCGTG	210	
QY	63	GCACCTGAGGCAAGCGGCTGACGCTACTGTGAGAGGAAAGAAAGTTGTGAGCAGCCCGCAGG	122	
Db	211	GCACCTGAGGCAAGCGGCTGACGCTACTGTGAGAGGAAAGAAAGTTGTGAGCAGCCCGCAGG	270	
QY	123	ACCCCTGGCCAGCCCTGAGCCCGCAGCGCTTGCGCGAGACCCCTGTGTGAGAGCAGAGCCAGT	182	
Db	271	ACCCCTGGCCAGCCCTGAGCCCGCAGCGCTTGCGCGAGACCCCTGTGTGAGAGCAGAGCCAGT	330	
QY	183	GAGCCCAAGTGAAGCAAGGCTGCTTGTGACGCCACCGGCTGTGACAATCAGAGAACCCCTCCAG	242	
Db	331	GAGCCCAAGTGAAGCAAGGCTGCTTGTGACGCCACCGGCTGTGACAATCAGAGAACCCCTCCAG	390	
QY	243	AGGCCATGAGACAGGCTGCGCCGCTGACGGCCAGGGTGAAGCATGTGAGAGATCGCCCGG	302	
Db	391	AGGCCATGAGACAGGCTGCGCCGCTGACGGCCAGGGTGAAGCATGTGAGAGATCGCCCGG	450	
QY	303	AGCCAAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATCACAAGAAATACACCACTTT	362	
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QY	363	GCAAAAGACATGAGAGGCCCATGTGCGTGTACATGCTGTGTGGCTTCGACTGCTGGCTCCATG	422	
Db	511	GCAAGACACATGAGAGGCCCATGTGCGTGTACATGCTGTGTGGCTTCGACTGCTGGCTCCATG	570	
QY	423	GGACCTGTGTGAGGCCCAGAGAGAAAGGTTTGAAGGCACTGAGAGAGGCTTCGCAAGAGAG	482	
Db	571	GGACCTGTGTGAGGCCCAGAGAGAAAGGTTTGAAGGCACTGAGAGAGGCTTCGCAAGAGAG	630	
QY	483	TTCAATTTAACTPAACAGGTACAAGCCGGCGGAGAGTCCACAGACAAATGCACCTAACCC	542	
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QY	543	TTCAATTTGCCCCAGACAGCGGGTCAACGGGTCCATCTTGCGTCAACTCCAAAGAGGCTGAG	602	
Db	691	TTCAATTTGCCCCAGACAGCGGGTCAACGGGTCCATCTTGCGTCAACTCCAAAGAGGCTGAG	750	
QY	603	GTCGTTCTCGAGAAACCAAGTGCATPAAGCAGGAGCTAAGCTGTCTCAAAATGAGCTGCTC	662	
Db	751	GTCGTTCTCGAGAAACCAAGTGCATPAAGCAGGAGCTAAGCTGTCTCAAAATGAGCTGCTC	810	
QY	663	AAGCAGAAAGCGGCAGATCGAGACCGCTGACAGAGCTGTGTGAAGGTGACAGCGCGCATTTGTG	722	
Db	811	AAGCAGAAAGCGGCAGATCGAGACCGCTGACAGAGCTGTGTGAAGGTGACAGCGCGCATTTGTG	870	
QY	723	AGCGAGGTGAAGCTGCTGCGCAGAGAGAGCCGCCAATCATGAATCTGCGGGTCAACGCAGCTC	782	
Db	871	AGCGAGGTGAAGCTGCTGCGCAGAGAGAGCCGCCAATCATGAATCTGCGGGTCAACGCAGCTC	930	

Db 331 GAGCCAGTGAAGGACAGGAGCTGTTGGCAGCACCAGGCTGCAACTGAGAACCCCTCCAG 390
QY 243 AGGCTATGACAGGCTGCCCCGCTGACGGCCAGAGTGAAGCATGTGAGAGCCGCCCG 302
Db 391 AGGCAATGACAGGCTGCCCCGCTGACGGCCAGAGTGAAGCATGTGAGAGCCGCCCG 450
QY 303 AGGCAAGCAGAGGAGAGAGGCTTTTATGATTTCTATTGACAAAGAAATAACACATTT 362
Db 451 AGGCAAGCAGAGGAGAGAGGCTTTTATGATTTCTATTGACAAAGAAATAACACATTT 510
QY 363 GCAAGACCATGAGGCACTGTGCTGCAATGTGTGTGCTGAGCTGTGCTGTGCATG 422
Db 511 GCAAGACCATGAGGCACTGTGCTGCAATGTGTGTGCTGAGCTGTGCTGTGCATG 570
QY 423 GGAAGCTGTGACAGGACAGAGAGCGGTTTGAAGGAGCAGAGAGGCTGCGCAAGAG 482
Db 571 GGAAGCTGTGACAGGACAGAGAGCGGTTTGAAGGAGCAGAGAGGCTGCGCAAGAG 630
QY 483 TTCAATTACCTAAACAGATACAGCGGCGGCGAGTCCAGAGACAAAGTGCCTTACACC 542
Db 631 TTCAATTACCTAAACAGATACAGCGGCGGCGAGTCCAGAGACAAAGTGCCTTACACC 690
QY 543 TTCAATTGTGCTGACAGAGGAGTCAAGGAGTGCCTTGTGCTGCACTTCCAGAGCTGAG 602
Db 691 TTCAATTGTGCTGACAGAGGAGTCAAGGAGTGCCTTGTGCTGCACTTCCAGAGCTGAG 750
QY 603 GTGCTTCTGAGAGACAGAGTGCATAGCAGAGAGCTGAGCTGCTCAACATGAGCTGCT 662
Db 751 GTGCTTCTGAGAGACAGAGTGCATAGCAGAGAGCTGAGCTGCTCAACATGAGCTGCT 810
QY 663 AAGCAGAGCGGAGATGAGAGCTGCAAGAGCTGCAAGAGTGAAGTGAAGCGGCGCATTTGT 722
Db 811 AAGCAGAGCGGAGATGAGAGCTGCAAGAGCTGCAAGAGTGAAGTGAAGCGGCGCATTTGT 870
QY 723 AGGAGATGAAGTGTGCGCAGAGAGAGCGGCAATGATGATGCGGCGGCTGCGCAGAGCT 782
Db 871 AGGAGATGAAGTGTGCGCAGAGAGAGCGGCAATGATGATGCGGCGGCTGCGCAGAGCT 930
QY 783 TACATGAGCTCTGACAGAGATCATCGCAGAGCGGAGCAAGCGTTGAGTCTTCCAG 842
Db 931 TACATGAGCTCTGACAGAGATCATCGCAGAGCGGAGCAAGCGTTGAGTCTTCCAG 990
QY 843 CTGAGAGACAGATCTGTGACAGAGACAGAGCGGAGATCTGTGCTGCGCAGAGTCAAG 902
Db 991 CTGAGAGACAGATCTGTGACAGAGACAGAGCGGAGATCTGTGCTGCGCAGAGTCAAG 1050
QY 903 GACCTGAGACAGATGACAGAGCTGCGCAGAGCTGCGCAGAGCAACATGAGAGATCATC 962
Db 1051 GACCTGAGACAGATGACAGAGCTGCGCAGAGCTGCGCAGAGCAACATGAGAGATCATC 1110
QY 963 GCGCAGCTTGAAGAGACATGCGCAGAGAGGCTGCTGCGCAGAGCGGCTGCGCAGAGCC 1022
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QY 1083 TCTACCAAGAGATCCAGAGTGAAGAGCTGAGAGGCTGCGCAGAGCGGCTGCGCAG 1142
Db 1231 TCTACCAAGAGATCCAGAGTGAAGAGCTGAGAGGCTGCGCAGAGCGGCTGCGCAG 1290
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Db 1291 ATGCGCAGCTGACAGAGCTGCGCAGAGCTGCGCAGAGCGGCTGCGCAGAGCGGCTGCG 1350
QY 1203 TGCTGACAGGCTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1262
Db 1351 TGCTGACAGGCTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1410
QY 1263 AATACCAAGCTGCTGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1322
Db 1411 AATACCAAGCTGCTGATGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1470

QY 1323 GTCAATCCAGAGACCGCTGAGATGCTCTGTTAATCTTCTGAGAGACAGAGAGACCTACAG 1382
Db 1471 GTCAATCCAGAGACCGCTGAGATGCTCTGTTAATCTTCTGAGAGACAGAGAGACCTACAG 1530
QY 1383 CAAGGCTTGGAGACATGACAGGAGATGCTGAGGCTGAGAGACATTTACTGAGCTG 1442
Db 1531 CAAGGCTTGGAGACATGACAGGAGATGCTGAGGCTGAGAGACATTTACTGAGCTG 1590
QY 1443 ACGAACCAAGCACTACAACTCTGCTGACATGAGAGCTGCTGCGCGCAGAGTGC 1502
Db 1591 ACGAACCAAGCACTACAACTCTGCTGACATGAGAGCTGCTGCGCGCAGAGTGC 1650
QY 1503 TTTGAGATATGAGCAGATTTCCGCTGAGAACCTGAGAGCAGATATTTAAAGCTGCGGCTG 1562
Db 1651 TTTGAGATATGAGCAGATTTCCGCTGAGAACCTGAGAGCAGATATTTAAAGCTGCGGCTG 1710
QY 1563 GGGGCTACCATGAGCAATGCGGAGTACTCTTTACATGAGCAACAGCGCAAGCACTTAC 1622
Db 1711 GGGGCTACCATGAGCAATGCGGAGTACTCTTTACATGAGCAACAGCGCAAGCACTTAC 1770
QY 1623 ACCCTGACAGAGATCATGATGCTGACAGAGAACTGTGCGCACTACAGAGAGGAGG 1682
Db 1771 ACCCTGACAGAGATCATGATGCTGACAGAGAACTGTGCGCACTACAGAGAGGAGG 1830
QY 1683 TGTGTGTAAAGCTGCTGAGCCTCAACCTCAACGAGGAGTCTGTACCGGCGGAGGCT 1742
Db 1831 TGTGTGTAAAGCTGCTGAGCCTCAACCTCAACGAGGAGTCTGTACCGGCGGAGGCT 1890
QY 1743 TACCGAGCGGCTACAGAGAGAGTCTA CTGGGCTGAGATTCGAGAGAGCTCTTACTCA 1802
Db 1891 TACCGAGCGGCTACAGAGAGAGTCTA CTGGGCTGAGATTCGAGAGAGCTCTTACTCA 1950
QY 1803 CTCAAGAAAGTGTGATGATGATCCAGACCGAACCTCAACCTTCACTAAGCAGCTCC 1862
Db 1951 CTCAAGAAAGTGTGATGATGATCCAGACCGAACCTCAACCTTCACTAAGCAGCTCC 2010
QY 1863 CCTCTGACCTCTGTGAGCATTGCGAGAGAGCCACCTGCTGACAGCTGCGCAGAGC 1922
Db 2011 CCTCTGACCTCTGTGAGCATTGCGAGAGAGCCACCTGCTGACAGCTGCGCAGAGC 2070
QY 1923 AAAAGAACACTCTCAGAGATTCATCTGAGAGCTGAGAGAGCGGAGATGCTGAGTTCGT 1982
Db 2071 AAAAGAACACTCTCAGAGATTCATCTGAGAGCTGAGAGAGCGGAGATGCTGAGTTCGT 2130
QY 1983 TTTCCGAAGTCACTGACAGCGGATGATGAACTGATGATGATGATGATGATGATGATGATGAT 2042
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QY 2043 TACTTTCTTCAACACAGAGAGCGGCTGATGCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 2102
Db 2191 TACTTTCTTCAACACAGAGAGCGGCTGATGCTTCCAGAGAGAGAGAGAGAGAGAGAGAG 2250
QY 2103 CTCTTTCTTAAATAATTAAGTCTCTACAAATAAACA 2141
Db 2251 CTCTTTCTTAAATAATTAAGTCTCTACAAATAAACA 2289

RESULT 9
US-10-140-808-267
; Sequence 267, Application US//10140808
; Publication No. US20030017563A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Wei-Oiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

QY 1263 AACACCAACCGCTCATGAGTGTGTGCGACAGAGACAGACCCCGGGGGCTGAGCC 1322
 DB 1411 AACACCAACCGCTCATGAGTGTGTGCGACAGAGACAGACCCCGGGGGCTGAGCC 1470
 QY 1333 GTGATCCAGAGAGCGCTGTGATGCTGTGTAATCTTTCAGAGAACTGGGAACTGTAAG 1382
 DB 1471 GTGATCCAGAGAGCGCTGTGATGCTGTGTAATCTTTCAGAGAACTGGGAACTGTAAG 1530
 QY 1383 CAAGGTTTGGGAACTGAGGCGGGAATAGTGGCTGGGCTGGAGAACTTATCTGAGCTG 1442
 DB 1531 CAAGGTTTGGGAACTGAGGCGGGAATAGTGGCTGGGCTGGAGAACTTATCTGAGCTG 1590
 QY 1443 ACGAACCAAGGCACTACAACTCTGTGACCATGAGAGAGTGTCCGGCCGCAAGTTC 1502
 DB 1591 ACGAACCAAGGCACTACAACTCTGTGACCATGAGAGAGTGTCCGGCCGCAAGTTC 1650
 QY 1503 TTTCAGAGAACTAGCCAGTTCCTGCTGGAACCTGAGACGAGTATTAATGCTGGGCTG 1562
 DB 1651 TTTCAGAGAACTAGCCAGTTCCTGCTGGAACCTGAGACGAGTATTAATGCTGGGCTG 1710
 QY 1563 GGGCGCTACCTAGTGCATGCGGATGACTCTTTTAACTAGGCAACGCGCAAGCACTTACC 1622
 DB 1711 GGGCGCTACCTAGTGCATGCGGATGACTCTTTTAACTAGGCAACGCGCAAGCACTTACC 1770
 QY 1623 ACCCTGAGACAGATCATGATGTCTTACAGAGAACTGTGCCACTTACCAAGAGGAGGC 1682
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 QY 1683 TGGTGTATTAACGCTGTGCTCCCACTCAACCTCAACGCGGATGTGTTACCGGGGGGCAAT 1742
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 QY 1803 CTCGAAGAAGTGTGATGATGATTCGAGACGGAACCCCAACCTTCCACTTAAGCCAGCTCC 1862
 DB 1951 CTCGAAGAAGTGTGATGATGATTCGAGACGGAACCCCAACCTTCCACTTAAGCCAGCTCC 2010
 QY 1863 CCCTCCTGACCTCTCTGCGCAATGCGAGAGCCCAACCTTGTCAAGCTGGCGACAGAC 1922
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 QY 1923 AAGAGCAACTCTCTCAACCGCTTCACTCTGAGGCTGGAGAGACCGGAGATCTGATCTGT 1982
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 QY 1983 TTCCGAGTCACTGAGGCGGATGATGAACTGAACTGATGAGTGTCTGTCTCTCTCC 2042
 DB 2131 TTCCGAGTCACTGAGGCGGATGATGAACTGAACTGATGAGTGTCTGTCTCTCTCC 2190
 QY 2043 TACTTCTCTTACACAGACAGGCGCTCACTGTCTCCAGAGACGAGACACTTACAGACAA 2102
 DB 2191 TACTTCTCTTACACAGACAGGCGCTCACTGTCTCCAGAGACGAGACACTTACAGACAA 2250
 QY 2103 CTCTTCTCTTAAATTAATTAAGTCTTACAAATTAATAA 2141
 DB 2251 CTCTTCTCTTAAATTAATTAAGTCTTACAAATTAATAA 2289

RESULT 11
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 ; Sequence 267, Application US/10127852A
 ; Publication No. US20030203428A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Geo, Mei-Qiang
 ; APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C08
 CURRENT APPLICATION NUMBER: US/10/127,852A
 PRIOR FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 267
 LENGTH: 2290
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-127-852A-267
 Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2135; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 3 AATGAGCTGCTGCGGACGCGCTTGAAGTGAACCCCAAGCCCTGAGCCTGCGAGCGTG 62
 DB 151 AATGAGCTGCTGCGGACGCGCTTGAAGTGAACCCCAAGCCCTGAGCCTGCGAGCGTG 210
 QY 63 GCACTGAGGAGCGGCTGAGCGTACTGTGAGGAGAAAGTGTGAGAGAGCCCGCAGG 122
 DB 211 GCACTGAGGAGCGGCTGAGCGTACTGTGAGGAGAAAGTGTGAGAGAGCCCGCAGG 270
 QY 123 ACCCTGAGCAAGCCCTGAGCCCAAGCTTCTGCGGAGCCCTCTGTGAGAGAGCCCAAGT 182
 DB 271 ACCCTGAGCAAGCCCTGAGCCCAAGCTTCTGCGGAGCCCTCTGTGAGAGAGCCCAAGT 330
 QY 183 GAGCCGAGTGAAGGAGGCTGTGAGGAGCCCAAGCTTCTGAGAGAGCCCTCTGAGAG 242
 DB 331 GAGCCGAGTGAAGGAGGCTGTGAGGAGCCCAAGCTTCTGAGAGAGCCCTCTGAGAG 390
 QY 243 AGGCAATGAGCAGGCTGCGCGCTGAGCGGCGAGGCTGAAGCATGTGAGAGAGCCCGCGG 302
 DB 391 AGGCAATGAGCAGGCTGCGCGCTGAGCGGCGAGGCTGAAGCATGTGAGAGAGCCCGCGG 450
 QY 303 AGCCAGCAGAGAGGAGAGGCTTCAATTAATTTCAAGAGATTAACCAATTTT 362
 DB 451 AGCCAGCAGAGAGGAGAGGCTTCAATTAATTTCAAGAGATTAACCAATTTT 510
 QY 363 GCAAGACCATGAGGCGCACTGTGTGTGATGATGCTGTGTGTGTGAGTGTGCTGCTGCA 422

PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 267
 LENGTH: 2290
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-127-900A-267

Query Match 98.1%; Score 2132.6; DB 13; Length 2290;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 215; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3 AATGAGGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 62
 151 AATGAGGCTGCTGCGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 210
 63 GCATGAGGAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 122
 211 GCATGAGGAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 270
 123 ACCCTGAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 182
 271 ACCCTGAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 330
 183 GAGCCAGTGAAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 242
 331 GAGCCAGTGAAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 390
 243 GAGCCAGTGAAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 302
 391 GAGCCAGTGAAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 450
 451 GAGCCAGTGAAGCGGCTGAGCGGCTGAGATGAACCCCAAGCCCTGAGCTGCGAGCGTG 510
 303 AGCCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 362
 451 AGCCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 510
 363 GCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 422
 511 GCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 570
 423 GCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 482
 571 GCAGGAGGAGGAGGCTTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 630
 483 TTCAATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 542
 631 TTCAATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 690
 543 TTCAATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 602
 691 TTCAATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTT 750
 603 GTGCTTCTGAGAACCGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCT 662

751 GTGCTTCTGAGAACCGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCT 810
 663 AAGCAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 722
 811 AAGCAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 870
 723 AAGCAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 782
 871 AAGCAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 930
 783 TACATGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 842
 931 TACATGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 990
 843 CTGAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 902
 991 CTGAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1050
 903 GACCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 962
 1051 GACCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1110
 963 GCGAGCTTGAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1022
 1111 GCGAGCTTGAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1170
 1023 CCGCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1082
 1171 CCGCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1230
 1083 TCTACAGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1142
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 1143 ATGCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1202
 1291 ATGCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1350
 1203 TGCCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1262
 1351 TGCCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1410
 1263 AACACCAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1322
 1411 AACACCAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1470
 1323 GTCAATGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1382
 1471 GTCAATGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1530
 1383 CAAGGAGTGAAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1442
 1531 CAAGGAGTGAAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1590
 1443 ACGAACCAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1502
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 1503 TTTGAGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1562
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 1563 GGGGCTTACAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1622
 1711 GGGGCTTACAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1770
 1623 ACCCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1682
 1771 ACCCTGAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1830
 1683 TGGTGTATTAAGGAGGAGTGCATTAAGCAAGGAGTGAAGCTGCTCAATGAGTCTGCTCAATGAGTCTGCTCAATGAGTCTGCT 1742

QY 843 CTGAGAAAGAGATCTGAAACGAGACGAGCATGCTGAGCTGGCCAGCAAGTACAG 902
DB 991 CTGAGAAAGAGATCTGAAACGAGACGAGCATGCTGAGCTGGCCAGCAAGTACAG 1050
QY 903 GACCTGGAGCAAGATACCAGCACTGGCCACACTGGCCCAACCAATCAGATGATC 962
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QY 1083 TGTACCAAGAGATCCAGAGTACAGCAAGCTGAAGTGTGGCCAGCCCTCTGCCCACT 1142
DB 1231 TGTACCAAGAGATCCAGAGTACAGCAAGCTGAAGTGTGGCCAGCCCTCTGCCCACT 1290
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QY 1203 TGGCTGGAGGCGCTGGAGGATGGCCAGCAACCACTCATCTGCTGTAAGCCGAG 1262
DB 1351 TGGCTGGAGGCGCTGGAGGATGGCCAGCAACCACTCATCTGCTGTAAGCCGAG 1410
QY 1263 AACACCAACCGCTCATGAGAGTGTGTGCAACAAGACAGACCCCGGCGCTGAGAC 1322
DB 1411 AACACCAACCGCTCATGAGAGTGTGTGCAACAAGACAGACCCCGGCGCTGAGAC 1470
QY 1323 GTGATTCAGAGAGCGCTGATGGCTGTGTAACTTCTCAGAGATGGGAGACGTAAG 1382
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QY 1383 CAGGGTTGGAGAACTTACAGCGCAATACTGGCTGGCCAGCAATTTACTGCGTG 1442
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DB 1651 TTGTCAGAGTACGCGGCTTCCGCTGGAGACTGAGAGAGTATTAAGTGGCGTG 1710
QY 1623 ACCCTGGAGAGATGATGATGTTTACAGAGAACTGGCCACTACCAAGAGGAGAGC 1682
DB 1711 GGGCGCTACCATGAGCATGCGGATGATCTTTACATGCAACAGGCAAGCATTCACC 1770
QY 1683 TGGTGGTATACGCGCTGTGCGCACTCAACCTCAACGAGGATGTGTACCGCGGGGCGCAT 1742
DB 1831 TGGTGGTATACGCGCTGTGCGCACTCAACCTCAACGAGGATGTGTACCGCGGGGCGCAT 1890
QY 1743 TACCGAGAGCGCTACAGAGAGAGTCTGCGGCTGAGTTCGAGAGAGGCGCTTACCA 1802
DB 1891 TACCGAGAGCGCTACAGAGAGAGTCTGCGGCTGAGTTCGAGAGAGGCGCTTACCA 1950
QY 1803 CTCAGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
DB 1951 CTCAGAGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010
QY 1863 CCGCTCTGAGCTCTGCGGCACTGCGAGAGCCAGCCCTGCTGACGCTGGCAAGCAGC 1922
DB 2011 CCGCTCTGAGCTCTGCGGCACTGCGAGAGCCAGCCCTGCTGACGCTGGCAAGCAGC 2070
QY 1923 AAGAGAACTCTCAACCAAGTCTGAGGCTGGAGAGAGCGGAGATCTGATTCGT 1982

DB 2071 AAGAGAACTCTCTCAACCAAGTCTGAGGCTGGAGAGAGCCGAGATCTGATTCGT 2130
QY 1983 TTTCGAGATCACTGAGAGGAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 2042
DB 2131 TTTCGAGATCACTGAGAGGAGTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAAT 2190
QY 2043 TACTTTCCTTCAACCAAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
DB 2191 TACTTTCCTTCAACCAAGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2250
QY 2103 CTCCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2141
DB 2251 CTCCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2289

RESULT 14
US-10-131-820A-267
Sequence 267, Application US/10131820A
Publication No. US20030203431A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C144
CURRENT APPLICATION NUMBER: US/10/131, 820A
PRIOR FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 267
LENGTH: 2290
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-820A-267

Query Match 58.1%; Score 2132.6; DB 13; Length 2290;
Best Local Similarity 99.8%; Pred. No. 0;

Db 1711 GGGCGCTACATGCGAATGCGGGTGCCTCTTACATGCGACAACGCGCAGAGTTACCC 1770
QY 1623 ACCGTGACAGAGATCATGATGTCTACACAGGAACCTGTGCCCCACTACACAGAGGAGGC 1682
Db 1771 ACCCTGACAGAGATCATGATGTCTACACAGGAACCTGTGCCCCACTACACAGAGGAGGC 1830
QY 1683 TGGTGGTAAACGCGCTGTGCCCCACTCAACCTCAACGCGGGTCTGGTACCGCGGGGCCAT 1742
Db 1831 TGGTGGTAAACGCGCTGTGCCCCACTCAACCTCAACGCGGGTCTGGTACCGCGGGGCCAT 1890
QY 1743 TACCGGAGCCGCTACACAGAGAGAGTCTACTGGGCTGAGTTCCGAGAGGCTTTACTCA 1802
Db 1891 TACCGGAGCCGCTACACAGAGAGAGTCTACTGGGCTGAGTTCCGAGAGGCTTTACTCA 1950
QY 1803 CTCAGAAAGTGTGATGATGATCCGACCGAACCCTCAACCTTCACTAAGCCAGCTCC 1862
Db 1951 CTCAGAAAGTGTGATGATGATCCGACCGAACCCTCAACCTTCACTAAGCCAGCTCC 2010
QY 1863 CCTTCTGACCTCTGTGGCCATTGCGAGAGCCCACTTGTGTCAGCTGGCCACAGCAC 1922
Db 2011 CCTTCTGACCTCTGTGGCCATTGCGAGAGCCCACTTGTGTCAGCTGGCCACAGCAC 2070
QY 1923 AAAGAACAACTCCTCAGCAGTTCACTGAGGCTGGAGAGACCGGAGTGTGATTTCTGT 1982
Db 2071 AAAGAACAACTCCTCAGCAGTTCACTGAGGCTGGAGAGACCGGAGTGTGATTTCTGT 2130
QY 1983 TTTCGAAAGTCACTGACGCGAGTGAATGAAATCGATACGGTGTCTGTCTCTCC 2042
Db 2131 TTTCGAAAGTCACTGACGCGAGTGAATGAAATCGATACGGTGTCTGTCTCTCC 2190
QY 2043 TACTTCTCTTACACAGACAGCCCTCATGTCTCCAGAGACAGACAGAGACTTACAGACA 2102
Db 2191 TACTTCTCTTACACAGACAGCCCTCATGTCTCCAGAGACAGACAGAGACTTACAGACA 2250
QY 2103 CTCTTCTTTAAATTAATTAAGTCTCTACAAATTAATAACA 2141
Db 2251 CTCTTCTTTAAATTAATTAAGTCTCTACAAATTAATAAAA 2289

Search completed: August 6, 2004, 20:44:37
Job time : 987 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2004, 13:47:28 ; Search time 5559 Seconds

(without alignments)
11673.056 Million cell updates/sec

Title: US-10-018-386-1

Perfect score: 2173
Sequence: 1 gaagaatgagctgctgcgcga.....aaaaaaaaaaaaaaaaaaaaa 2173

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estin:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1345.4	61.9	2062	11	AK037265	AK037265 Mus muscu
2	1039.4	47.8	1201	9	AL527015	AL527015 AL527015
3	989.6	45.5	1201	9	AL523842	AL523842 AL523842
4	939.8	43.2	1201	9	AL572386	AL572386 AL572386

Result 1	Score	Match	Length	DB	ID	Description
5	931.8	42.9	3560	11	AK041888	AK041888 Mus muscu
6	908.6	41.8	1201	9	AL547465	AL547465 AL547465
7	885.2	40.7	1201	9	AL546299	AL546299 AL546299
8	873.8	40.2	1201	9	AL54832	AL54832 AL54832
9	870.6	40.1	1111	12	BM906705	BM906705 AGENCOURT
10	865.4	39.8	929	13	BQ711105	BQ711105 AGENCOURT
11	865	39.8	881	13	BQ879104	BQ879104 AGENCOURT
12	826.8	38.0	1195	9	AL525269	AL525269 AL525269
13	825.2	38.0	884	13	BQ852353	BQ852353 AGENCOURT
14	817.4	37.6	1201	9	AL527059	AL527059 AL527059
15	816.4	37.6	870	14	CD515651	CD515651 AGENCOURT
16	777.2	35.8	797	14	CF131488	CF131488 UI-HF-PO
17	777	35.8	875	13	BQ659478	BQ659478 AGENCOURT
18	767.6	35.3	2306	11	AK011976	AK011976 Mus muscu
19	759.6	35.0	1201	9	AL523843	AL523843 AL523843
20	739.6	34.0	949	12	B1834238	B1834238 603084145
21	733.2	33.7	812	12	B1765043	B1765043 603051189
22	732.8	33.7	752	13	BQ717905	BQ717905 AGENCOURT
23	726.6	33.4	915	13	BQ149131	BQ149131 AGENCOURT
24	724.8	33.4	945	13	BQ713459	BQ713459 AGENCOURT
25	715.8	32.9	720	14	CF132047	CF132047 UI-HF-PO
26	714.8	32.9	941	10	BF038654	BF038654 601460914
27	704.4	32.4	822	10	BF345980	BF345980 602018709
28	701	32.3	990	10	BE745986	BE745986 601573433
29	691.6	31.8	700	12	BG676460	BG676460 602622918
30	686.6	31.6	738	12	B1768582	B1768582 603056901
31	677	31.2	683	13	BX482997	BX482997 DKF2D686B
32	671.4	30.9	682	14	CA411602	CA411602 UI-HF-EU1
33	659.6	30.4	666	12	CF131252	CF131252 UI-HF-PO
34	659	30.3	880	12	BG818186	BG818186 602779784
35	657.4	30.3	673	13	BQ574556	BQ574556 UI-H-EZ1
36	653.2	30.1	825	13	BU053122	BU053122 UI-M-FCO
37	643.4	29.6	667	13	BU624314	BU624314 UI-H-FG1
38	632.4	29.1	795	14	CF724071	CF724071 UI-M-GZO
39	611	28.1	946	10	BF038016	BF038016 601461729
40	610.8	28.1	749	12	BM007984	BM007984 603617732
41	607.4	28.0	819	10	BF348335	BF348335 60202367
42	593	27.3	667	12	BG819300	BG819300 602781481
43	582.4	27.2	881	14	CB193085	CB193085 AGENCOURT
44	591.8	27.2	646	12	BM999031	BM999031 UI-H-DIO
45	574.2	26.4	762	14	CK019588	CK019588 AGENCOURT

ALIGNMENTS

RESULT 1
AK037265
LOCUS
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
enriched library, clone:AL30002A02 product:ANGIOPOTENIN-RELATED
PROTEIN 2 PRECURSOR, full insert sequence.

ACCESSION AK037265
VERSION AK037265.1 GI:26332039
KEYWORDS
SOURCE HTC; CAP trapper.
MUS musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636-
AUTHORS
TITLE
JOURNAL Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
MEDLINE 20499374
PubMed 11042159

REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PubMed 10349636-
AUTHORS
TITLE
JOURNAL Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
MEDLINE 20499374
PubMed 11042159

REFERENCE
AUTHORS

3 Shihata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carinci, P., Komoro, H., Akiyama, J., Nishi, K., Katsunaka, T., Teshiro, H., Itoh, A., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED

20530913
11076861

REFERENCE
AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

REFERENCE
AUTHORS

5 (bases 1 to 2062)
6 Aizawa, K., Aizawa, K., Akimura, T., Arai, A., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koyama, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohtsuo, N., Okaaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shihata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyu, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, Fax: 81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

1. 2062

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428. 1909

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CDS

ORIGIN

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Matches 1589; Conservative 0; Mismatches 261; Indels 37; Gaps 5;

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DEFINITION	AL527015 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED				
ACCESSION	AL527015				
VERSION	AL527015.2				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Li, M.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	1 (bases 1 to 1201)				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001) On Feb 13, 2001 this sequence version replaced gi:12790508. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4821.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DC017CF02NP1&cluster=4821.r. Contact : Feng Liang Email : fliang@life.techn.com URL : http://fulllength.invitrogen.com/Invitrogen_Corporation_1600_Faraday_Avenue_Genoscope_sequence_ID : CS0DC017CF02NP1. Location/Qualifiers				
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 DB 25 AGTATCTAAATTAATAANVAVM 4

RESULT 3
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 LOCUS AL523842 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DC003YP19 3-PRIME, mRNA sequence.
 ACCESSION AL523842
 VERSION AL523842.2 GI:31042103
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 13, 2001 this sequence version replaced gi:12787335.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

FEATURES
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 Location/Qualifiers

ORIGIN
 Query Match 45.5%; Score 989.6; DB 9; Length 1201;
 Best local Similarity 91.6%; Pred. No. 1,8e-121;
 Matches 1030; Conservative 37; Mismatches 53; Indels 4; Gaps 3;

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 QY 1672 AGAAGGAGGCTGTGTATTAAGCTGTGCCACTTCAACCTCAACGCGGCTGTGTACC 1731

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 4821.r. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC003CH1ONP1&cluster=4821.r. Contact:
 Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID: CS0DC003CH1ONP1.
 Location/Qualifiers

Db 464 AGAAGGAGAGCTGGTGTATTAACGCTGTGCCACTCAACCTCAACGAGGAGTCTGTGTACC 405

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Qy 1792 GCTCTTACTACTCAAGAAAGTGTATGATGATCCGACGGAACCCCAACACTTCCACT 1851

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Db 164 CTGGAATCTGTTTCCGAGATCTGACGAGGATGATGGAATGATGATGATGATGATG 105

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Db 104 TGTGCTCTCTCTACTCTTCTTCAACACAGAGCCCTCATGTCCTCAAGACAGACAG 45

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Db 44 ACTACAGACAG 1

RESULT 4

AL572386/c 1201 bp mRNA linear EST 31-MAY-2003

LOCUS AL572386 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

DEFINITION clone CS0D1011YPI4 3-PRIME, mRNA sequence.

ACCESSION AL572386

VERSION AL572386.2 GI:31293769

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 1201)

Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:12930602.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4821.r For more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1011DH07NPL&cluster=4821.r. Contact: Feng Liang Email: fliang@life.techn.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Paraday Avenue Genoscope sequence ID: CS0D1011DH07NPL.

FEATURES

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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BclI V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 43.2%; Score 939.8; DB 9; Length 1201;

Best Local Similarity 89.0%; Pred. No. 6.7e-115;

Matches 1031; Conservative 37; Mismatches 82; Indels 9; Gaps 6;

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Qy 1106 CCAGAACCTGAAGTGTGTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165

Db 1036 CMA--AACCTGAAGTGTGTCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980

Qy 1166 ATCTTCAACGCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1225

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Qy 1226 CCAGACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1284

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Qy 1405 GCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1464

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Qy 1465 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1524

Db 679 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 620

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Db 319 CCGACCGAAGCCCAACCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 260

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Db 259 TTGCGAG 200

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Db 199 CATCTGAG 140

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Oy	2065	CCCCATCATGTCTCCAGACAGACAGACAGACTACAGACACTCTTTCTTTTAATAATTAA	2124
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Oy	2125	TCTTCACTATTAATAACACA	2143
Dd	20	NCACAKAAANKKAATVAMM	2
RESULT 5			
AKO41888			
LOCUS			
DEFINITION	AKO41888	3560 bp	mRNA linear HTC 19-SEP-2003
VERSION	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A63004F14 product:ANGIOPOIETIN-RELATED PROTEIN 2 PRECURSOR, full insert sequence.		
KEYWORDS	AKO41888		
SOURCE	AKO41888 1 GI:26088710		
ORGANISM	HTC; CAP trapper.		
REFERENCE	Mus musculus (house mouse)		
AUTHORS	Eutheria; Euterazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Carninci P. and Hayashizaki Y.		
JOURNAL MEDLINE	High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS	2		
TITLE	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M. and Hayashizaki Y.		
JOURNAL MEDLINE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	2049374		
REFERENCE	11042159		
AUTHORS	3		
TITLE	Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuma T., Teshiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazana M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwagi K., Fujiwase S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M., Yoshida Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kiria A. and Hayashizaki Y.		
JOURNAL MEDLINE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicephillary sequencer Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	20530913		
REFERENCE	11076861		
AUTHORS	4		
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
JOURNAL MEDLINE	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)		
PUBMED	5		
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)		
TITLE	Nature 420, 563-573 (2002)		
JOURNAL MEDLINE	6 (bases 1 to 3560)		
PUBMED	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T., Horii F., Imomani K., Ishii Y., Itoh M., Kagawa I., Kakikawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koyu S., Kuritara C., Matsuyama T., Miyazaki A., Murita M., Nakamura M., Nishi K., Nomura K., Nunazaki R., Ono N., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N.,		

	TITLE	Sano,H., Saeki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
	JOURNAL	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, 1-7-22 Suehiro-dcho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsic.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
	COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encycloipedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/. Location/Qualifiers
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	Matches 1149; Conservative	0; Mismatches 217; Indels 37; Gaps 5,
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QY	102	GATTGTGAGCACCCCGCAGAGACCCTTGCCAGCCCTTGCGCCAGCTCTGCCGAGCCC 161
DB	166	GATTGGAGCAGCCCCGGGTGACACACAGAGCAGCCTCATCCCTTAGAGACTTCAGAGACA 225
QY	162	TCTGTGAGAGAGACCGACGTGAGACCCGACGTAGGACAGGGCGTTGGAGACCA--CGGC 219
DB	226	TAGACTG----CTGCCAGCTGTAGCGCAGTAGAGAGGGCGTCTCGGCGCCAATCTCAAC 280
QY	220	CTGCACACTCAGAAAACCCCTCCACAGAGGCCATGACAGGCTGCCCGCTGACGCGCAGGGTG 279
DB	261	CTGAGACTCGGAACTCTCTCTGAGAGGCCACGCGGACGAGCTGTGCTGTATGG-CACCGTG 339
QY	280	AAGCATGTGAGAGCGCCCGCGAGACCAAGACGAGAGGGAAGAGCTTTCATAGATTCTAT 339
DB	340	AGGCATGTGAAGCCGTGCTCCAGGGCCCAAGACGAGAGAAAGAGGCTTCA-----GT 391
QY	340	TCACAAAGATTAACACCATTTTGAAGAAGCATATAGGCCACTGTGCTGACATGCTGT 399
DB	332	TCTATAAACCAACACGACACTGTGAAGAGCATATAGGCCACTGTGTATGACTACTGGT 451

Page 7

DEFINITION	AL547465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone GS01011HP14 5-Primer, mRNA sequence.
ACCESSION	AL547465
VERSION	AL547465.1
KEYWORDS	EST.
SOURCE	AL547465.2 GI:31269296
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1201) Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12881558. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seq@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4821.r For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=GS01011DH070P1&cluster=4821.r. Contact : Feng Liang Email : fliang@life.com URL : http://fulllength.invitrogen.com/InvitrogenCorporation1600 Faraday Avenue Genoscope sequence ID : GS01011DH070P1.
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ORIGIN	Query Match Best Local Similarity 91.7%; Pred. No. 8,9e-111; Matches 991; Conservative 30; Mismatches 52; Indels 7; Gaps 5 41.8%; Score 908.6; DB 9; Length 1201; 423 GAGCGTTGTGAGGCGCAGAGGACGGTTTGAAGGAGCACTGAGAGGCGCTCGCAGAAG 482

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DEFINITION clone CS0D1031YF21 5-PRIME, mRNA sequence.
ACCESSION AL546299
VERSION AL546299.2 GI:31268133
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li M.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12879279.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4821.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1031YF21&cluster=4821.r. Contact:
Feng Liang Email: fliang@life.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
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ORIGIN
Query Match 40.7%; Score 885.2; DB 9; Length 1201;
Best Local Similarity 90.3%; Pred. No. 1.1e-107;
Matches 914; Conservative 34; Mismatches 63; Indels 1; Gaps 1;

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Qy 123 ACCCTGAGAGCGGCTGAGCGGCTGAGATGAACCCAGCCCTGACCTGCGAGCGTG 182
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REFERENCE 1 (bases 1 to 1111).
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 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
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<http://image.llnl.gov>
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 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb. Insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 036."

ORIGIN

Query Match 40.1%; Score 870.6; DB 12; Length 1111;
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QY 3 AAATGAGCTGCTGCGGAGAGCCCTGAGATGAACCCCAAGCCCTGAGCTGCCAGCTG 62
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 REFERENCE 1 (bases 1 to 929)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
 Plate: LLM2382 row: a column: 15
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 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

Query Match 39.8%; Score 865.4; DB 13; Length 929;
 Best Local Similarity 97.6%; Pred. No. 4,9e-105;
 Matches 908; Conservative 0; Mismatches 19; Indels 3; Gaps 3;

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DB 61 CCCAGGACAGTGCACCTACCTTATGTCGCCAGAGAGGGGTCAAGGGTGCATCT 120
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DB 121 GGGTCACTCCAAAGAGAGCTGAGTGTCTTGAGAGAACGAGTGCATAGCAGAGTAG 180
QY 640 AGCTGCTCAACATAGAGTGTCTTGAGAGAACGAGTGCATAGCAGAGTAG 699
DB 181 AGCTGCTCAACATAGAGTGTCTTGAGAGAACGAGTGCATAGCAGAGTAG 240
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DB 241 TGAAGTGAAGCGGCGGCTGAGGAGAGTGAAGTGTGAGCAAGAGAGAGCGGCA 300
QY 760 TGAAGTGAAGCGGCGGCTGAGGAGAGTGAAGTGTGAGCAAGAGAGAGCGG 819
DB 301 TGAAGTGAAGCGGCGGCTGAGGAGAGTGAAGTGTGAGCAAGAGAGAGCGG 360
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QY 940 CCCACACCATATCAGAGATATCGGCGAGTGAAGAGATCGGCGAGTGCCTTGG 999
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QY 1000 CCAGGCGGCTCCCGCAGAGCGGCGGCTGAGGAGAGTGAAGTGAAGTGAAG 1059
DB 541 CCAGGCGGCTCCCGCAGAGCGGCGGCTGAGGAGAGTGAAGTGAAGTGAAG 600
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DB 601 ACAACCGCATATCAACAGATCTTACCAAGATCCAGATCCAGATCCAGATCC 660
QY 1120 TGCCTGCAACCGGCTGAGGAGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGA 1179
DB 661 TGCCTGCAACCGGCTGAGGAGATGAGGAGTGAAGTGAAGTGAAGTGAAGTGA 720
QY 1180 AGCGGTGAGGCGCATGAGAGAGTGCCTGAGAGCGGCTGAGAGAGTGCCTG 1239
DB 721 AGCGGTGAGGCGCATGAGAGAGTGCCTGAGAGCGGCTGAGAGAGTGCCTG 780
QY 1240 CCATCTACTGTTGAAGCGGAGAGACCAACCGGCTATGAGAGTGTGTGAGAG 1299
DB 781 CCATCTACTGTTGAAGCGGAGAGACCAACCGGCTATGAGAGTGTGTGAGAG 838
QY 1300 GACAGAGCCCGGAGGCTGAGAGCGGCTATGAGAGACCGGCTATGAGAGTGT 1358

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DB 839 GACAGAGCCCGGAGGCTGAGAGCGGCTATGAGAGAGCGGCTGAGAGTGT 898
 QY 1359 TTGAGAGTGTGAGAGAGTATGAGAGAGG 1388
 DB 899 TTGAGAGTGTGAGAGAGTATGAGAGAGG 928

RESULT 11

B0879104

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Agencourt 8118172 Lupski dorsal root ganglion Homo sapiens cDNA
 clone IMAGE:6181203 5', mRNA sequence.
 B0879104.1 GI:22271112
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: sgabbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM3565 row: d column: 04
 High quality sequence stop: 671.
 Location/Qualifiers
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 /clone="IMAGE:6181203"
 /sex="male"
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 /dev_stage="adult, 36 yr"
 /lab_host="DH10a"
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 /note="Vector: pCMV-Sport6 (Life Technologies); Site_1:
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 5'-TCGACCCAGCGCTCCG-3' and
 5'-GACTAGTTTGAATGCGAGCGGCGGCTT(15)-3'. Size selected >
 1 kb for average insert length 1.7 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine) and is available through Life
 Technologies."

FEATURES

source

ORIGIN

Query Match 39.8%; Score 865; DB 13; Length 881;
 Best Local Similarity 98.9%; Pred. No. 5,6e-105;
 Matches 871; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 90 TGAGGAGAAAGAGTTGTGAGAGAGCGGCGAGAGCGGCTGAGGAGCGGCTG 149
DB 61 TGAGGAGAAAGAGTTGTGAGAGAGCGGCGAGAGCGGCTGAGGAGCGGCTG 120
QY 150 CTGCGGAGCGCTCTGTGAGAGAGAGAGCGAGAGCGGCTGAGGAGCGGCTG 209
DB 121 CTGCGGAGCGCTCTGTGAGAGAGAGAGCGAGAGCGGCTGAGGAGCGGCTG 180

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	Query Match	38.0%; Score 826.8; DB 9; Length 1195;
	Best Local Similarity	86.2%; Pred. No. 5,7e-100;
	Matches	859; Conservative 76; Mismatches 58; Indels 4; Gaps 4;
QY	1160 CCTCCCATCTTTCACCGACAAGCGGTGGGCCCCATGAGAAGACTGCCTGCAGGCCCTCGA	1219
Db	995 SCTCCCAATTTCACACCPACAA-SCTGSGSCCATTGAAXAAATCCCTGCAGGCCCTCGW	937
QY	1220 GGATGACCACGACACAGCTCCATCTACCTGGTAAGCCGGAAGAACCAACGCGCTCAT	1279
Db	936 GGWTGBCTACTACACCAAGCTCCATSTRYYTGTMAGCCCKMGWTAACMAACSCCTCAT	877
QY	1280 GCAGGTGTGTCGACCAAGACACACACCCCAGGGGGCTGGAACGCTATCCAGAGAGCCCT	1339
Db	876 KCAAGSKKT-GKGCAMAMADAPACAGACCCCGGGKGCTGGACSTCATCCAGAGACCT	818
QY	1340 GGATGCGCTGTGTACTTTCTTCAGAACTGGGAGACTACAGCAAGGAGGTTTGGAAACAT	1399
Db	817 GSATGSGCTCTGTACTTTCTTCAGTCTTAGTACAGCAAGCAAGGATTTGGGACAT	758
QY	1400 TGACGGCGAATACTGGGCTGGGCTTGGAACATTTACTGGCTGACCAACCAAGGCACTA	1459
Db	757 TGAACGGGAATACTGGGCTGGGCTTGGAACATTTACTGGCTGACCAACCAAGGCACTA	698
QY	1460 CAACCTCCGTGTGACCAATGAGAGACTGATCGGCGCGCAAGTCTTCAGATATCGGCAG	1519
Db	697 YAKAYTCTGTGTGACCAATGAGAGACTGATCGGCGCGCAAGTCTTCAGATATCGGCAG	638
QY	1520 TTTCGCGCTGAGACCTGAGACGAGTATTTAAGCTGCGGCTGGGGGCTTACATGGCAA	1579
Db	637 TTTCGCGCTGAGACCTGAGACGAGTATTTAAGCT-TTTTGKCGGGGTTACATGGCAA	579
QY	1580 TGCGGGTGAATCTCTTTTCAATGGCAACGGAACAGTTCACCAACCTCGACAGATATCA	1639
Db	578 TKCGGGTGAATCTCTTTTCAATGGCAACGGAACAGTTCACCAACCTCGACAGATATCA	519
QY	1640 TGATGTCTACACAGAAAATCTGTGCCACTACAGAAAGGAGGCTGTGTATTAAGCCTG	1699
Db	518 KGATGTCTACACAGAAAATCTGTGCCACTACAGAAAGGAGGCTGTGTATTAAGCCTG	459
QY	1700 TGCCCACTTCCAACCTCAACGGGGTCTGGTACCGGGGGGCGCATTAACGGAGCGGCTTACA	1759
Db	458 TGCCCACTTCCAACCTCAACGGGGTCTGTACTACGCGGGGCCCATTAACKGAGCCGCTATYA	399
QY	1760 GAGCGAGATCTACGGGCTGAGTTCCAGAGAGGCTCTTACTCACTCAAGAAAGTGAT	1819
Db	398 GAGCGAGATCTATTTGGGCKGAGKKYCAATAGTCTTACATCTTAAGAAAGTKTGAT	339
QY	1820 GATGATTCGACCGAACCACCAACCTTCTCAATTAAGCAAGTCTCCCTCTCTAAGTCTCGT	1879
Db	338 GATGATTCGACCGAACCACCAACCTTCTCAATTAAGCAAGTCTCCCTCTCTAAGTCTCGT	279
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Query Match	38.0%;	Score 825.2;	DB 13;	Length 884;
Best Local Similarity	98.0%;	Pred. No. 1e-99;		
Matches 866;	Conservative 0;	Mismatches 15;	Indels 3;	Gaps 3;

100

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1201)
AUTHORS Li W.B., Gruber, C., Jesse, J. and Polyses, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:12790552.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4821.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC017CF020P1&cluster=4821.r. Contact :
Peng Jiang Email : fjiang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0DC017CF020P1.
Location/Qualifiers

FEATURES
source

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/clone="CS0DC017Y103"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
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sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 37.6%; Score 817.4; DB 9; Length 1201;
Best Local Similarity 92.3%; Pred. No. 1e-98;
Matches 956; Conservative 29; Mismatches 37; Indels 14; Gaps 12;

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QY 63 GCACTGAGGACAGCGCTGACGCTACTGTGAGGAAAGAGTTGTGACAGACCCCGCAGG 122
DB |||||
QY 148 GCACGAGGACAGCGCTGACGCTACTGTGAGGAAAGAGTTGTGAGAGCAACCCCGCAGG 207
DB |||||
QY 123 ACCCTGGCCAGGCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAG 182
DB |||||
QY 208 ACCCTGGCCAGGCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAGCCCTGAG 267
DB |||||
QY 183 GAGCCAGTGAAGGAGGAGGCTGCTTGGAGCC-ACCGGCTGCAACTCAGAACCCCTTCA 241
DB |||||
QY 268 GAGCCAGTGAAGGAGGAGGCTGCTTGGAGCC-ACCGGCTGCAACTCAGAACCCCTTCA 327
DB |||||
QY 242 GAGCCAGTGAAGGAGGAGGCTGCTTGGAGCC-ACCGGCTGCAACTCAGAACCCCTTCA 301
DB |||||
QY 328 GAGCCAGTGAAGGAGGAGGCTGCTTGGAGCC-ACCGGCTGCAACTCAGAACCCCTTCA 387
DB |||||
QY 302 GAGCCAGTGAAGGAGGAGGAGGCTTTCATAGTTCTATTCAAAAGATAACACCAATT 361
DB |||||
QY 388 GAGCCAGTGAAGGAGGAGGAGGCTTTCATAGTTCTATTCAAAAGATAACACCAATT 447
DB |||||
QY 362 TGCAAGAACATGAGGAGGAGGAGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 421
DB |||||
QY 448 TGCAAGAACATGAGGAGGAGGAGGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 507
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QY 422 GGG-AGCTGTTGCAAGGC-AGGAGAGCGTTTGGAGGCG-ACTAGAGAGGCTGGCAAG 478
DB |||||
QY 508 GGGAGAGCTGTTGCAAGGC-AGGAGAGCGTTTGGAGGCG-ACTAGAGAGGCTGGCAAG 567
DB |||||
QY 479 AGAGTTCAATTTACTTAAACAGGTACAGCGGCGGCGAGTCCAGAGCAAGTCACTCA 538
DB |||||
QY 568 AGAGTTCAATTTACTTAAACAGGTACAGCGGCGGCGAGTCCAGAGCAAGTCACTCA 627
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QY 539 CACCTTCATTTGCTCCAGAGGAGGAGGCTGAGGAGGAGTCCATTCGCTCAACTCCAGAGGCC 598
DB |||||
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DB 628 CACCTTCATTTGCTCCAGAGGAGGAGGCTGAGGAGGAGTCCATTCGCTCAACTCCAGAGGCC 687
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DB 599 TGAGGAGCTTCTGAGAGAACCGAGTGCATPAGAGAGGAGGCTGCTCAACATAGAGT 658
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DB 688 TGAGGAGCTTCTGAGAGAACCGAGTGCATPAGAGAGGAGGCTGCTCAACATAGAGT 747
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DB 748 GCTCAAGCAGAACCGGACATGAGACGCTGAGAGGAGTGTGAAAGTGTGAGCGGAGT 807
QY |||||
DB 719 TGTGAGAGGAGTGTGAGAGTGTGCTGCGAGAGAGCCCGCAACATGAACTGCGGAGTCA 778
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DB 808 TGTGAGAGGAGTGTGAGAGTGTGCTGCGAGAGAGCCCGCAACATGAACTGCGGAGTCA 866
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DB 779 GCTTCATGAGTGTGCTGCTGCAAGAGTATCGGAGAGCGAGCAACAGGCTTGTGAGCTCTC 838
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DB 867 GCTTCATGAGTGTGCTGCTGCAAGAGTATCGGAGAGCGAG-MAAGGTTGAGCTCTC 924
QY |||||
DB 839 CCAAGTGTGAGAACAGATCTTGAACACAGACCGGACATGCTGCGAGTGTGAGAGT 898
QY |||||
DB 925 CCAAGTGTGAGAACAGATCTTGAACACAGACCGGACATGCTGCGAGTGTGAGAGT 983
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QY |||||
DB 1041 TATCGCGAGTGTGAGAGGAGTGTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1097
QY |||||
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QY |||||
DB 1098 CCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1113
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RESULT 15
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LOCUS
DEFINITION AGENCOURT_14366052 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30408400 5', mRNA sequence.
CD516561
CD516561.1 GI:31448279
EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ND4491 row: e column: 17
High quality sequence stop: 692.
Location/Qualifiers

FEATURES
source

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Mon Aug 9 10:30:09 2004

us-10-018-386-1.rst

Page 15

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(Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 37.6%; Score 816.4; DB 14; Length 870;
Best Local Similarity 98.9%; Pred. No. 1.5e-98;
Matches 843; Conservative 0; Mismatches 6; Indels 3; Gaps 2;

Search completed: August 6, 2004, 18:16:03
Job time : 5573 secs

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841 GGATCTTGAACC 852

